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## the pig as a biomedical model for human cutaneous melanoma : the MeLiM strain

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# The Pig as a biomedical model for human cutaneous melanoma : The MeLiM strain



**Génétique Animale et Biologie Intégrative  
Team : Genetics, Microbiota & Health**

**Giorgia Egidy Maskos Ph.D.**



**New challenges for animal sciences  
Jouy-en-Josas**

- ❖ Introduction on GABI – INRA, GeMS team
- ❖ Facts on cutaneous melanoma, therapies
- ❖ Animals models of melanoma
- ❖ Malignant melanoma traits in Minipigs MeLiM
- ❖ MeLiM, a model for successful cancer regression
- ❖ Animal Welfare



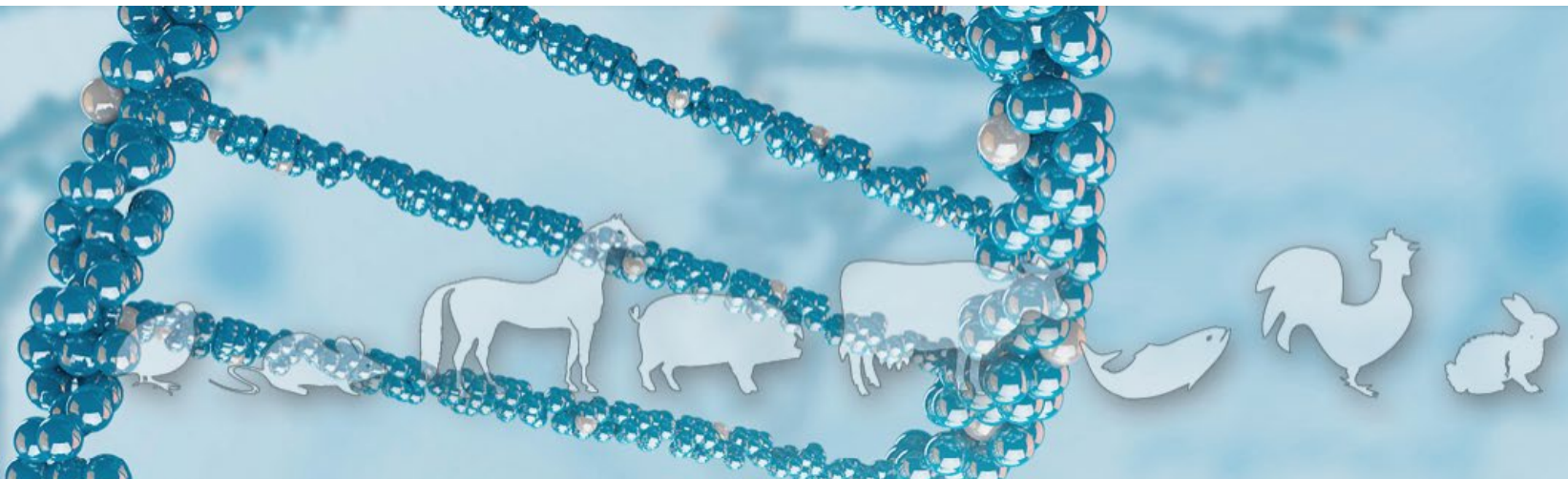
# GENETIQUE ANIMALE ET BIOLOGIE INTEGRATIVE

[http://www6.jouy.inra.fr/gabi\\_eng](http://www6.jouy.inra.fr/gabi_eng)

**GABI develops research on the characterisation and exploitation of genetic variability of animals for efficient and sustainable breeding**

**Studies focus on:**

- **Fundamental research on farm animals and model animals**
- **Applied research on breeding, genetic improvement**



# Genetics, Microbiota, Health team : GeMS

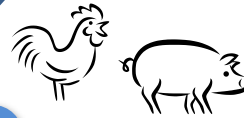
Swine  
experimental unit

@Bridge facility  
histology  
CRB GADIE

Genetics  
Genomics

Immunity

intestinal  
Microbiota

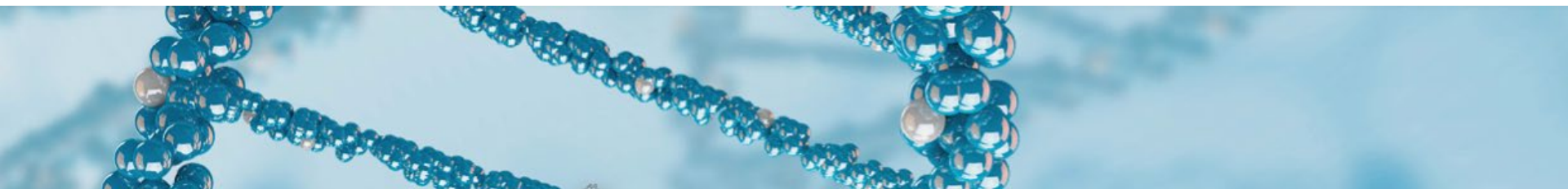


The Animal: an holobiont

Animal as  
livestock

Health

Animal  
models



# Genetics, Microbiota, Health team : GeMS

Collaboration **INRA** / **BGI-Shenzen** /  
**Copenhagen University**

- 7,7 millions genes, 719 MGS
- race, sex, age Influences
- Abundance of antibiotic resistance genes according to countries

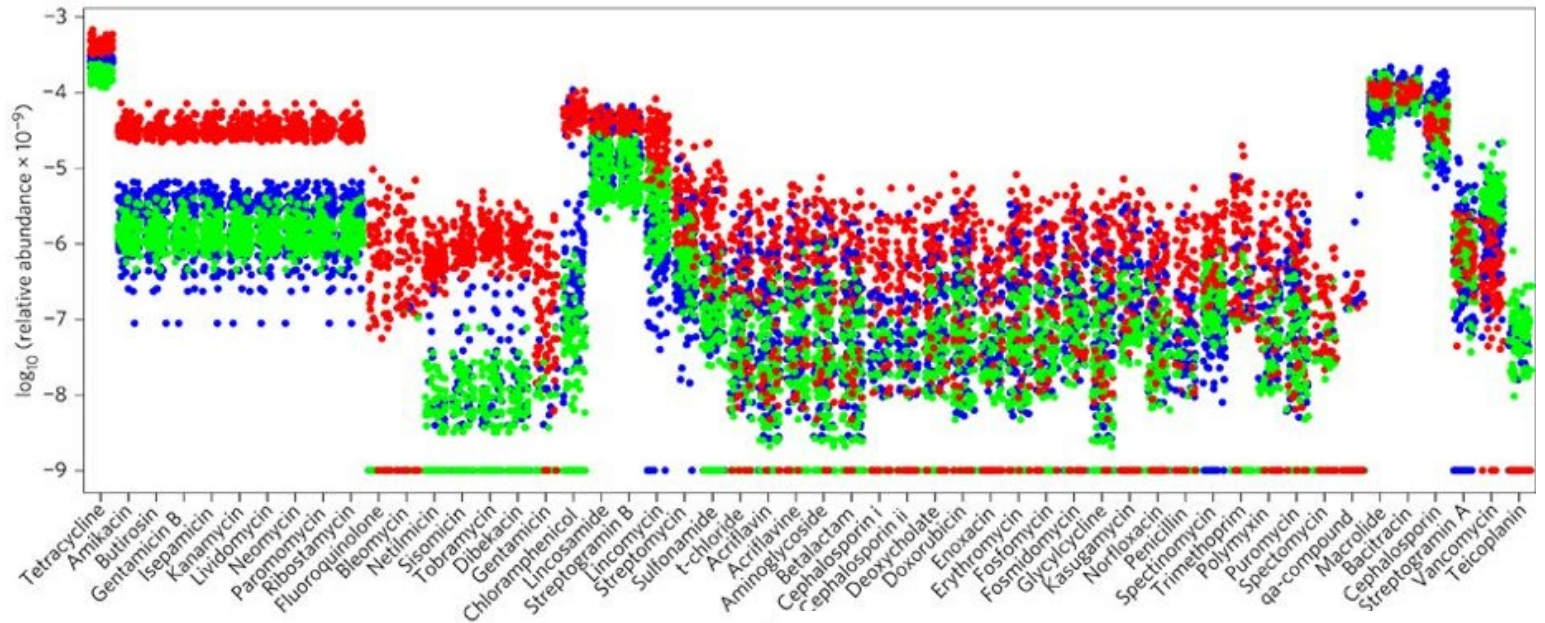
nature  
microbiology

PUBLISHED: 19 SEPTEMBER 2016 | ARTICLE NUMBER: 16161 | DOI: 10.1038/NMICROBIOL.2016.161

LETTERS

## A reference gene catalogue of the pig gut microbiome

Liang Xiao<sup>1†</sup>, Jordi Estellé<sup>2†</sup>, Pia Kählerich<sup>3†</sup>, Yuliaxis Ramayo-Caldas<sup>2</sup>, Zhongkui Xia<sup>1</sup>, Qiang Feng<sup>1‡</sup>, Suisha Liang<sup>1</sup>, Anni Øyan Pedersen<sup>4</sup>, Niels Jørgen Kjeldsen<sup>4</sup>, Chuan Liu<sup>1,5</sup>, Emmanuelle Maguin<sup>6</sup>, Joël Doré<sup>6,7</sup>, Nicolas Pons<sup>7</sup>, Emmanuelle Le Chatelier<sup>7</sup>, Edi Prifti<sup>7‡</sup>, Junhua Li<sup>1,8</sup>, Huijue Jia<sup>1</sup>, Xin Liu<sup>1</sup>, Xun Xu<sup>1</sup>, Stanislav D. Ehrlich<sup>7,9</sup>, Lise Madsen<sup>1,3,10</sup>, Karsten Kristiansen<sup>1,3,\*</sup>, Claire Rogel-Gaillard<sup>2,\*</sup>



Xiao, Estellé et al, Nature Microbiol. 2016

# Genetics, Microbiota, Health team : GeMS

## Towards the quantitative characterisation of piglets' robustness to weaning: a modelling approach

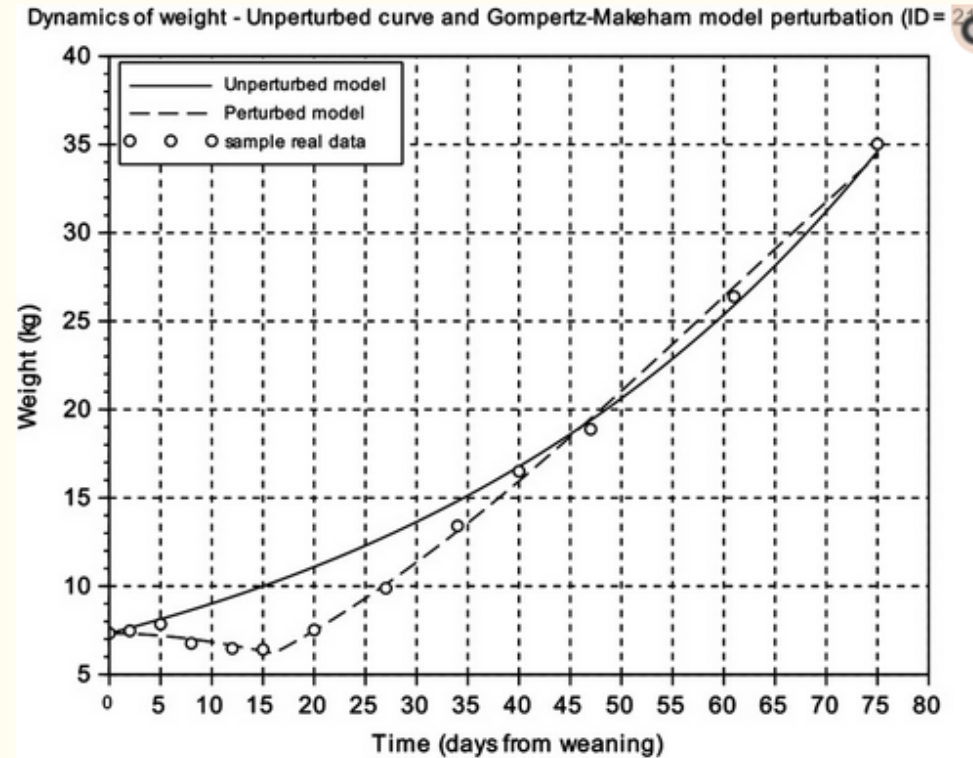
Collaboration UMR MoSAR

R Munoz-Tamayo

N Friggens

Comparison of the weight dynamics as predicted by the unperturbed and the perturbed (Gompertz–Makeham) models

- o different BW measures of the individual piglet relative to days from weaning
- the predicted response of the unperturbed growth model
- the perturbed growth model response



Revilla *et al* Animal, 2019

# Genetics, Microbiota, Health team : GeMS



A coordinated international action to accelerate genome to phenome

About FAANG

Structure

Activities

Data and Tools

To participate

more ▾

## FAANG Aims:

- Standardize core assays and experimental protocols
- Coordinate and facilitate data sharing
- Establish an infrastructure for analysis of these data
- Provide high quality functional annotation of animal genomes

## Working groups

- 🚩 **Steering Committee**
- ⚙️ Scientific Advisory Group
  - 📄 Animals, Samples, and Assays (ASA)
  - 📄 Bioinformatics and Data Analysis (B&DA)
  - 📄 Communication (COM)
  - 📄 Metadata and Data Sharing (M&DS)

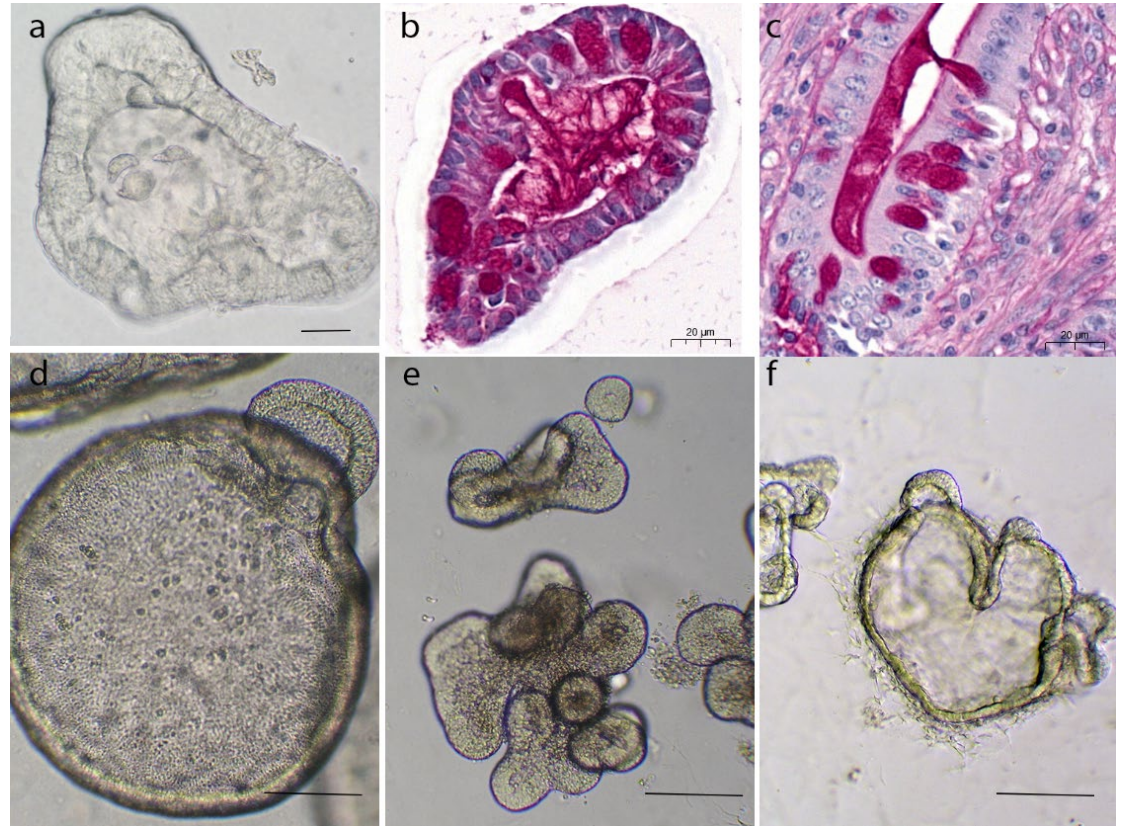
Giuffra & Tuggle, Annu Rev Anim Biosci 2019



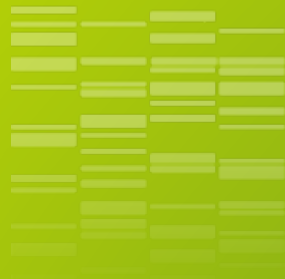


## Gut organoids

- Obtained from embryonic cells, iPSC, and adult stem cells from any organ
- Near physiological models to dissect complex traits into molecular phenotypes in a reproducible manner
- Biobanking friendly
- Powerful ethical compliant research platform for G-P in livestock & in vivo phenotyping : 3R



Pig tissues: a, b: ileum organoid, c: original tissue staining  
d: colon organoid, e: duodenum organoid, f: lung organoid



# Pigs as biomedical models

## Skin colour :



## Coat colour :



# Cutaneous melanoma in Man : Public health concern

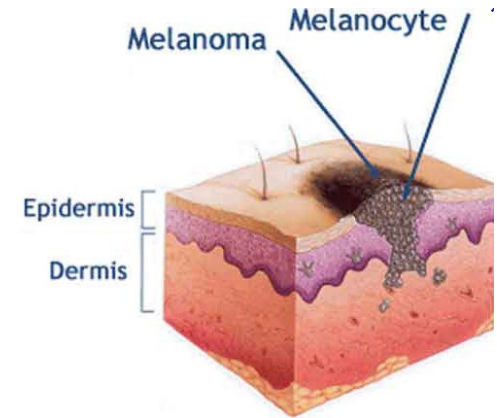
- Malignant tumour derived from melanocytes
- Highest rise in incidence rates since 1970
- 133 000 new cases/year (1500 in France)
- <5% of cutaneous cancer but 83% deaths
- 1st most common cancer in 25-30 years old group
- 90% sporadic, 10% familial occurrence

## Risk factors:

Environment : exposure to UV radiation, photo

host : genetic background, nb of nevi, skin ty

*CDKN2A, CDK4 (40% familial cases), MC1R (low risk)*



Intermittent exposure, chronically sun damaged skin or not!



# Cutaneous melanoma : diagnosis

By Donna Moncivaiz, March 30, 2015 at 9:16 am

## Clinical heterogeneity

ABCDE rule: JAMA (2004), 292:2776



Image courtesy of Healthwise, Incorporated and NCI Visuals Online

Combined neoplasms are often observed

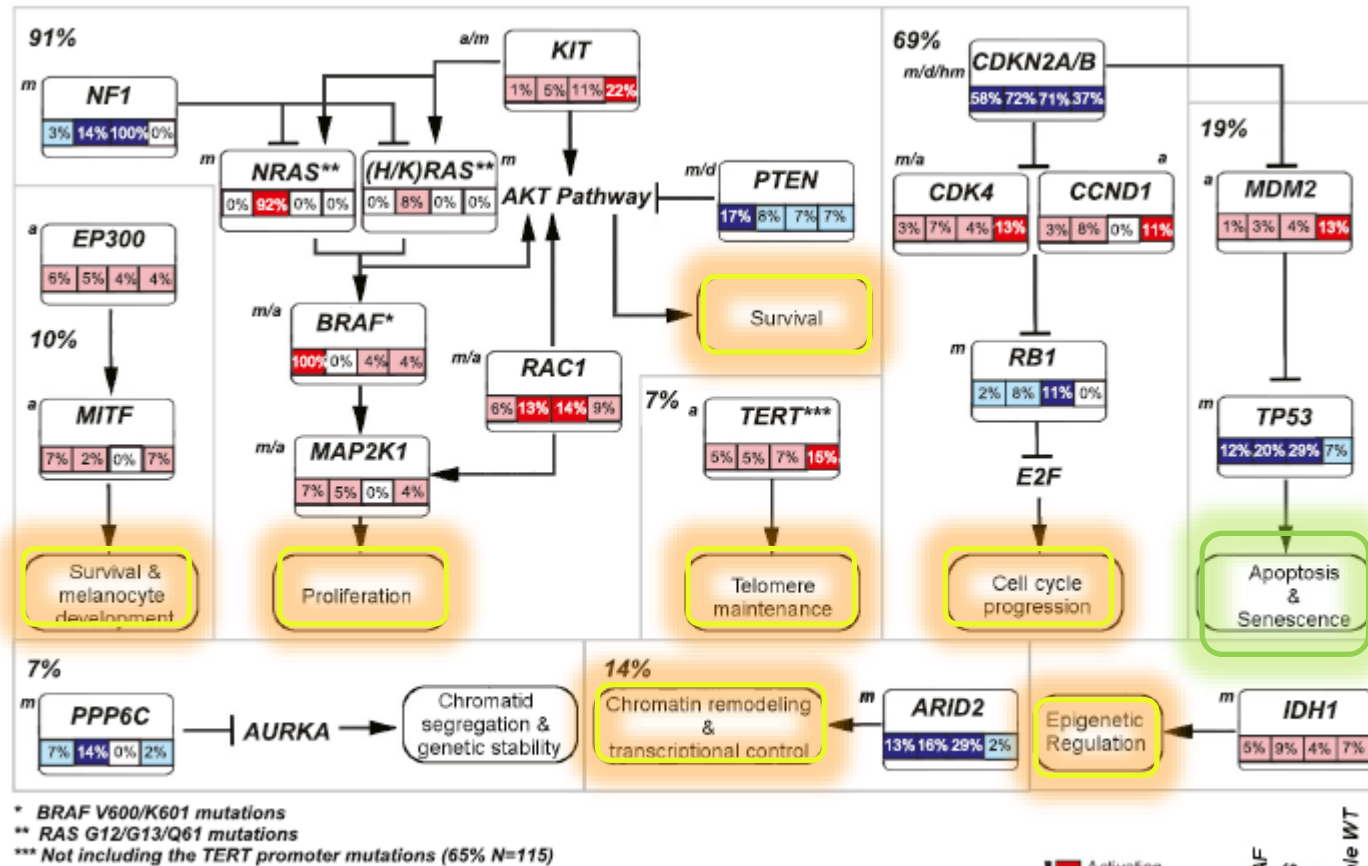
Melanoma can have many different appearances



Photo website Utah research center

# Genomic classification of cutaneous melanoma

The Cancer Genome Atlas Network, Cell 161: 1681, 2015



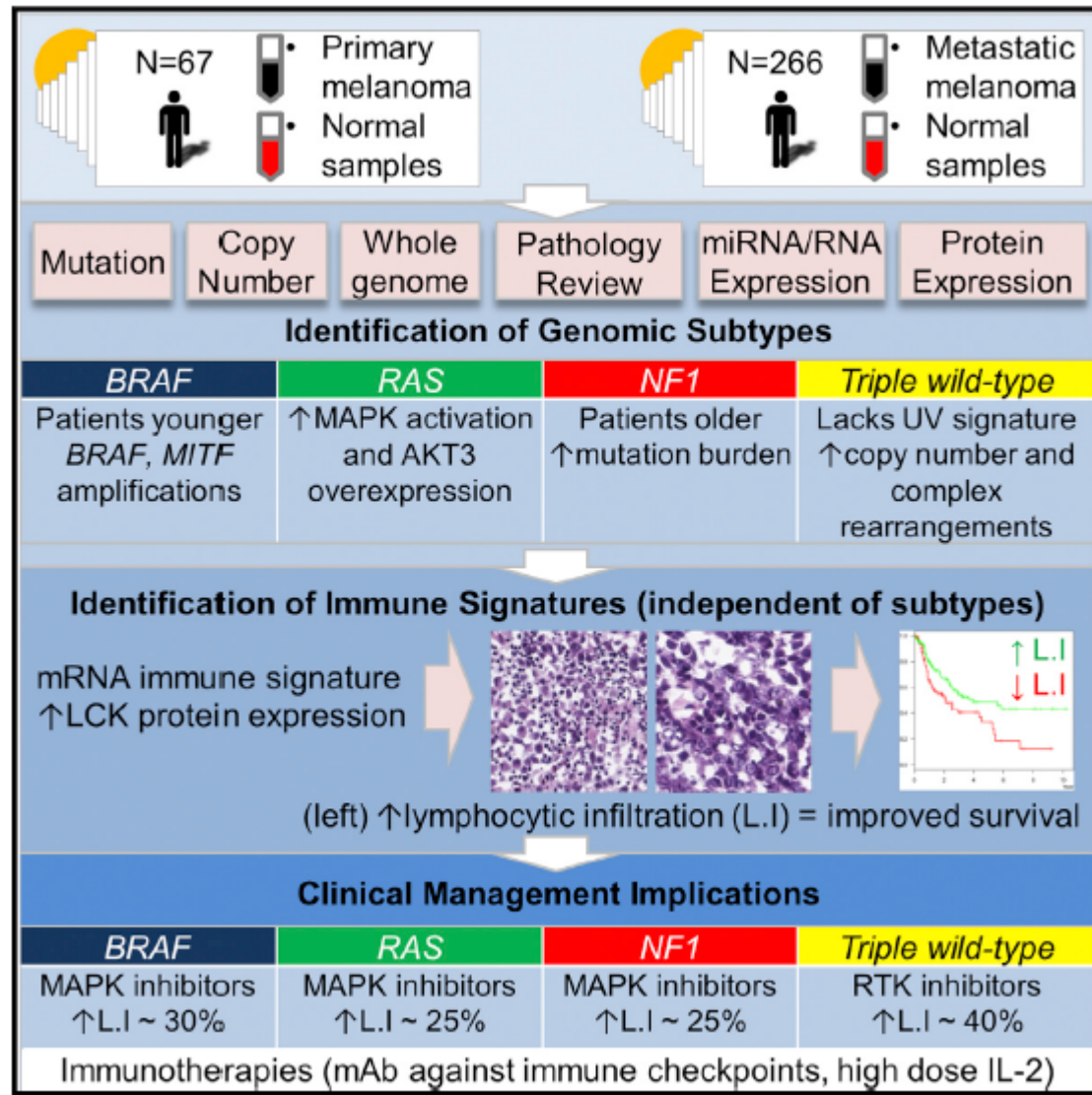
Pathways altered in melanoma:

Multiple linear canonical cascades converge to consolidate autonomous cell proliferation.

Cancer regression would gain from reactivation of apoptosis and senescence.

# Genomic classification of cutaneous melanoma

The Cancer Genome Atlas Network, Cell 161: 1681, 2015



Prognosis correlated only to tissue lymphocytic infiltration

# Available treatments

1. Excision surgery  
4 Stages I & II : no metastases → Excision 😊  
III & IV : metastases detected → bad prognosis
2. Chemotherapies : (dacarbazine) low response rates and low survival

3. New therapeutic strategies :

## **Gene targeted therapies** : Kinase inhibitors

- a. BRAF inhibitors (vemurafenib, dabrafenib, sorafenib)
- b. MEK inhibitors (trametinib)

rapid response, last 6-9 months, need other therapies

side effects: arthralgia, fatigue, nausea, rashes, photosensitivity, keratoacanthoma, pyrexia

## **Stimulation of immune responses:** Immune checkpoint blockers

Benefit only 15% of patients but no available biomarker to identify them

- a. Anti Cytotoxic T-lymphocyte-associated antigen-4 (CTLA-4) antibody (ipilimumab)
- b. Programmed-death-1 (PD1) (nivolumab) and its ligand (PD1L) (pembrolizumab)

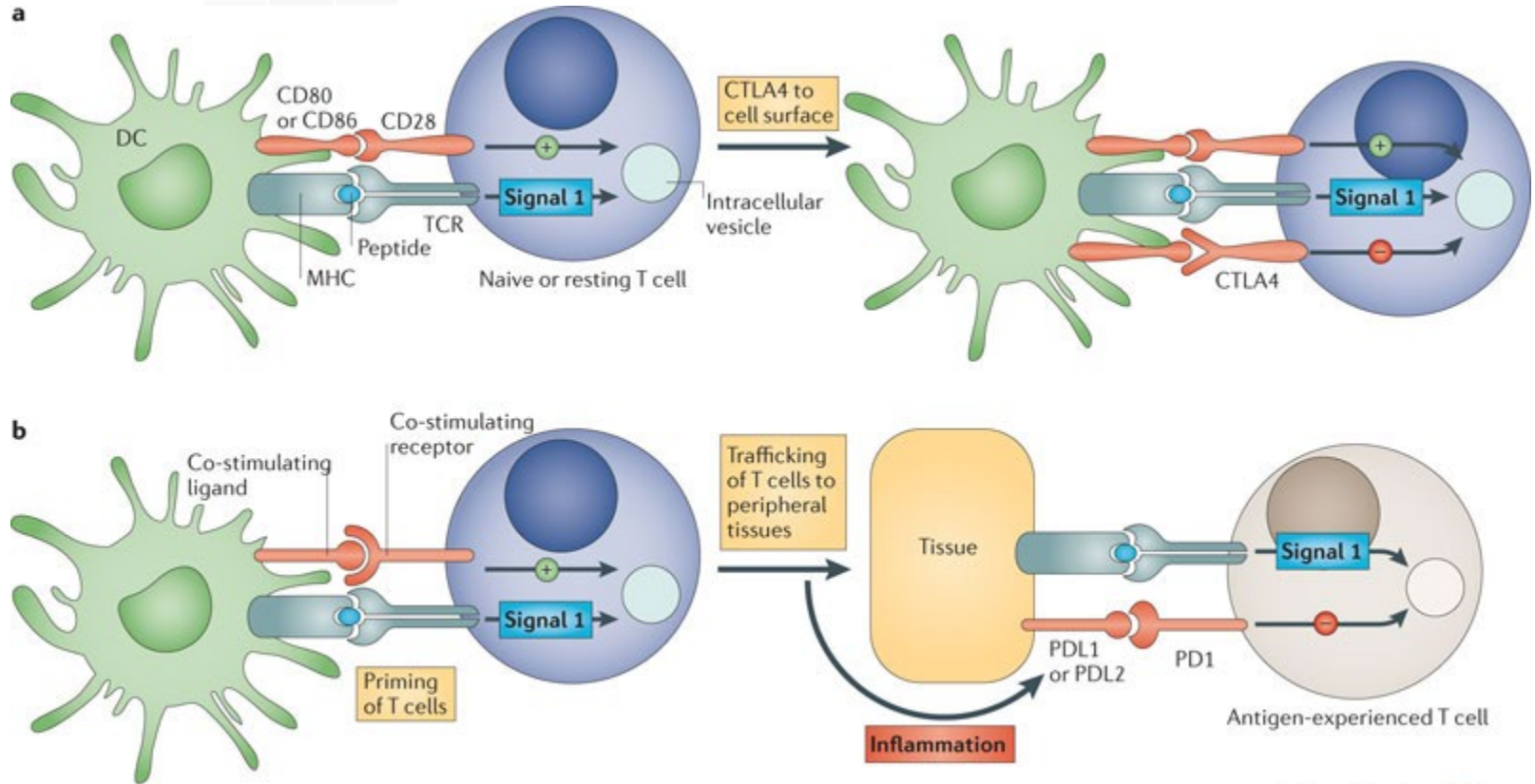
Slow but long term remission up to 5 years

side effects: toxicity to the bowel, lung and liver with potential life-threatening colitis, pneumonitis, hepatitis, need high doses steroids, fatigue, skin rashes, vitiligo





# Immune checkpoints regulate different components in the evolution of an immune system



Nature Reviews | Cancer

# Non human spontaneous melanoma models

## Induced

### By UV / carcinogens

Xyphophorus, opossum, mouse, hamster, rat, guinea pig, gerbil

### By transgenesis

Mouse

## Spontaneous

Xyphophorus (rare)

Rats (2-4%)

Hamster

Horse (80% grey horses >15 years old)

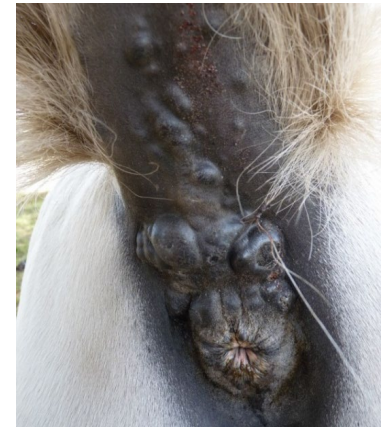
Dog (4-10%)

Angora Goat (rare)

Cattle (< 2%)

Cat (1%)

**Pigs**



**Perineal melanoma Grey horse**

Source : [www.nadis.org.uk](http://www.nadis.org.uk)



**Dog mouth melanoma**

Source : Unité d'histologie et d'anatomie pathologique, ENVA

Animal models are a good opportunity to study oncogenesis, for testing new therapeutic approaches

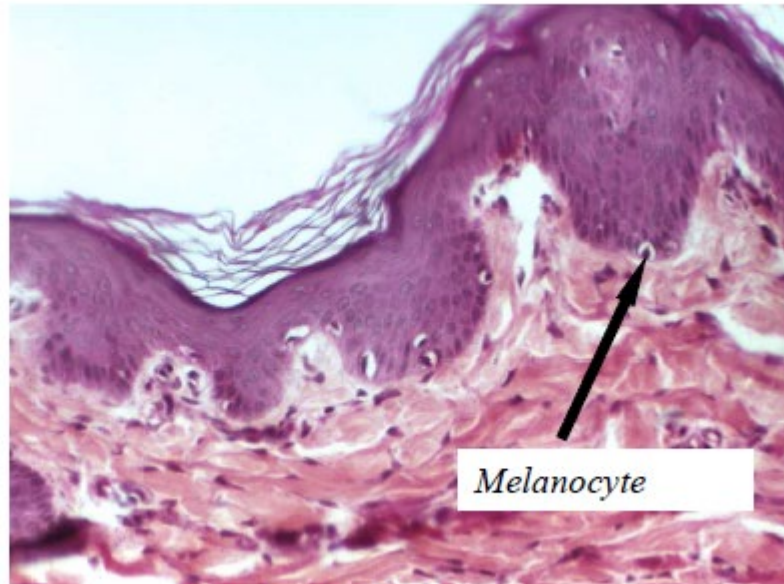
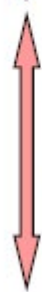
# Pig skin models human skin

Similar : organisation (dermis and stratified epidermis)  
position of melanocytes  
amounts of hair

Epidermis



Dermis



Pig skin- HESColoration - x20

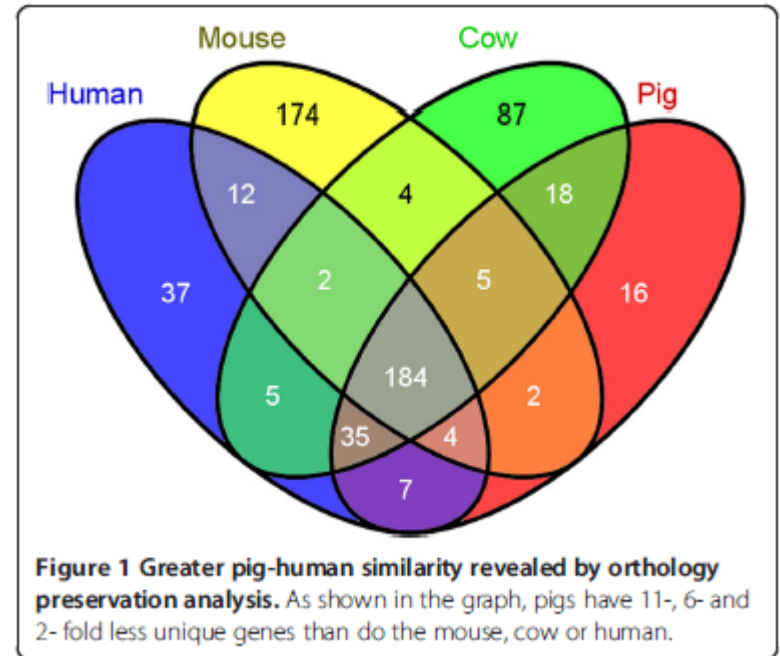
Pig skin offers a well-developed model for skin pathologies, including melanoma

# Pig immune system models human's

Swine immunome 2013:

Pigs & humans share 42 genes not found in mice  
Mice & humans share 14 genes not found in pigs

Frequency of gross protein structural preservation between human and pig for immune related genes is nearly twice that of mouse to human and pig to mouse (Dawson et al, 2016)



Dawson et al., BMC Genomics 2013

# Melanoma development in MeLiM

## Inherited

3 types of pigmented cutaneous lesions:  
flat, raised and small, exophytic melanoma

**Outbreak:** *in utero* or during the first 3 months

**Localisation :** variable

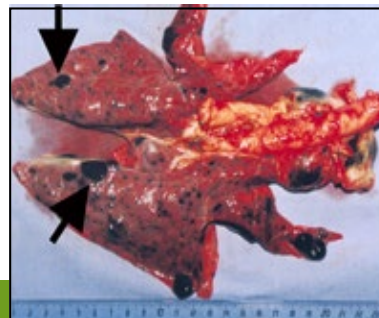
**Multiple lesions :** frequent

**Ulceration :** frequent

**Metastases :** draining lymph nodes, lungs,  
spleen, liver, digestive tract only on melanoma  
affected pigs

**Mortality:** 4%

Lung melanoma  
metastases in a  
young MeLiM

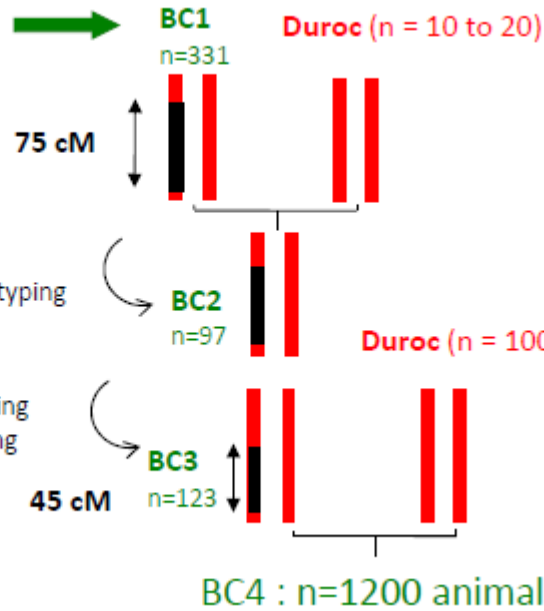


Vincent-Naulleau *et al* PCR 2004

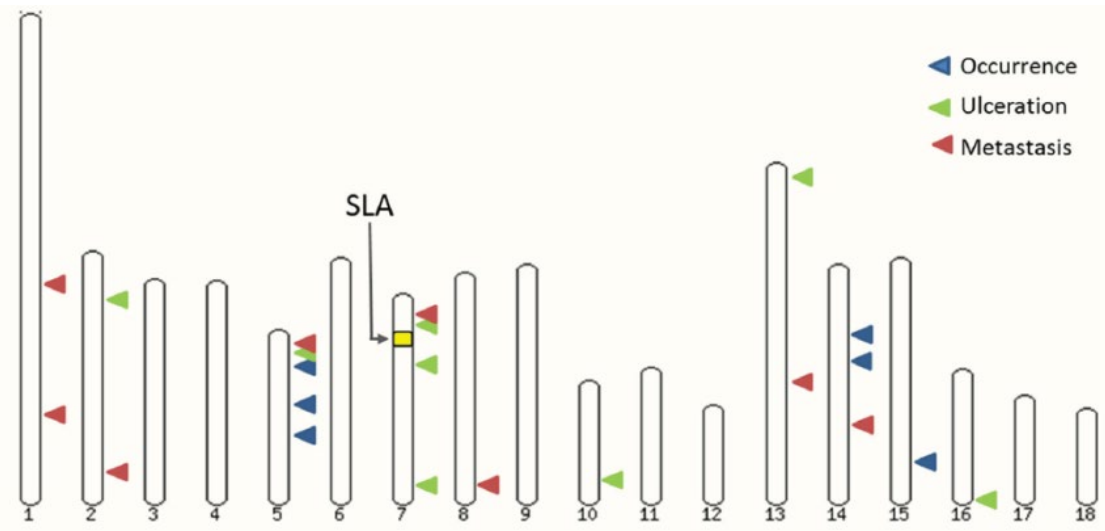
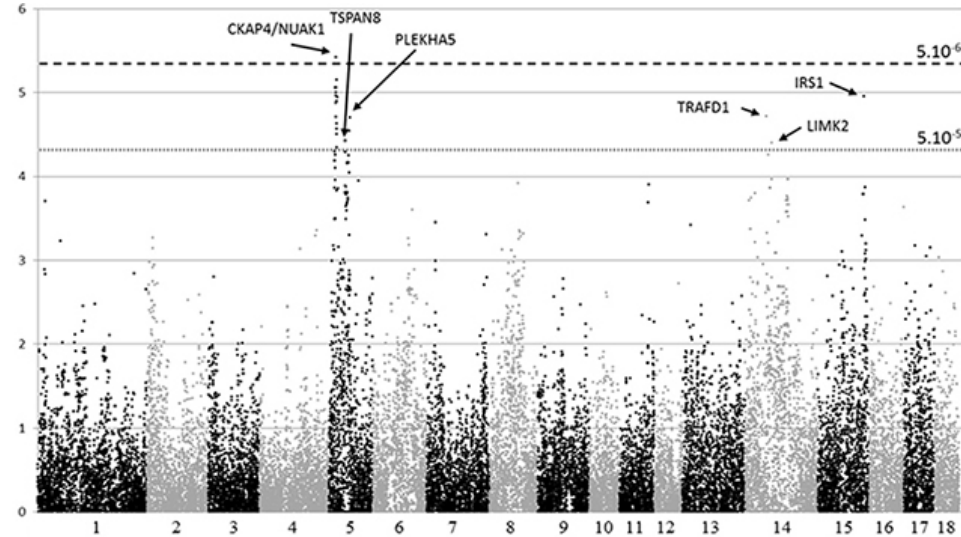
# Genome wide association study in MeLiM

4 MeLiM x 5 Duroc

9 affected F1



GWAS / 200 BC4 healthy vs melanoma

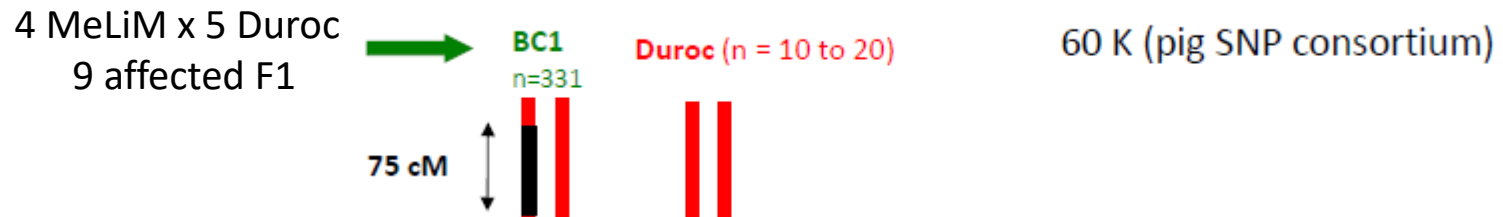


Bourneuf *et al*, Oncotarget 2018

# Genetic studies in MeLiM Candidate genes:

Human candidate gene sequencing on QTL detected by linkage analysis did not reveal causative mutations on MeLiM melanoma development: *CDKN2A*, *CDK4*, *MITE*, *KIT* (Le Chalony et al 2003, Bourneuf *et al* 2011, Fernandez-Rodriguez et al, 2014)

## Genome wide association study in MeLiM



Loci associated with phenotypes rare or difficult to measure in patients

Example: **Clinical ulceration** of tumors for which lack of clinical data, small cohorts  
In pig, association of ulceration with BPAG1-e gene ( $p$  corrected =  $2,75 \cdot 10^{-5}$ )



### BPAG1-e Restricts Keratinocyte Migration through Control of Adhesion Stability

Magdalene Michael<sup>1,2,3</sup>, Rumena Begum<sup>1,2</sup>, Kenneth Fong<sup>2</sup>, Celine Pourreyrone<sup>4</sup>, Andrew P. South<sup>4</sup>, John A. McGrath<sup>2</sup> and Maddy Parsons<sup>1</sup>

*Journal of Investigative Dermatology* (2014) 134, 773–782; doi:10.1038/jid.2013.382; published online 17 October 2013

Bourneuf *et al*,  
Oncotarget 2018



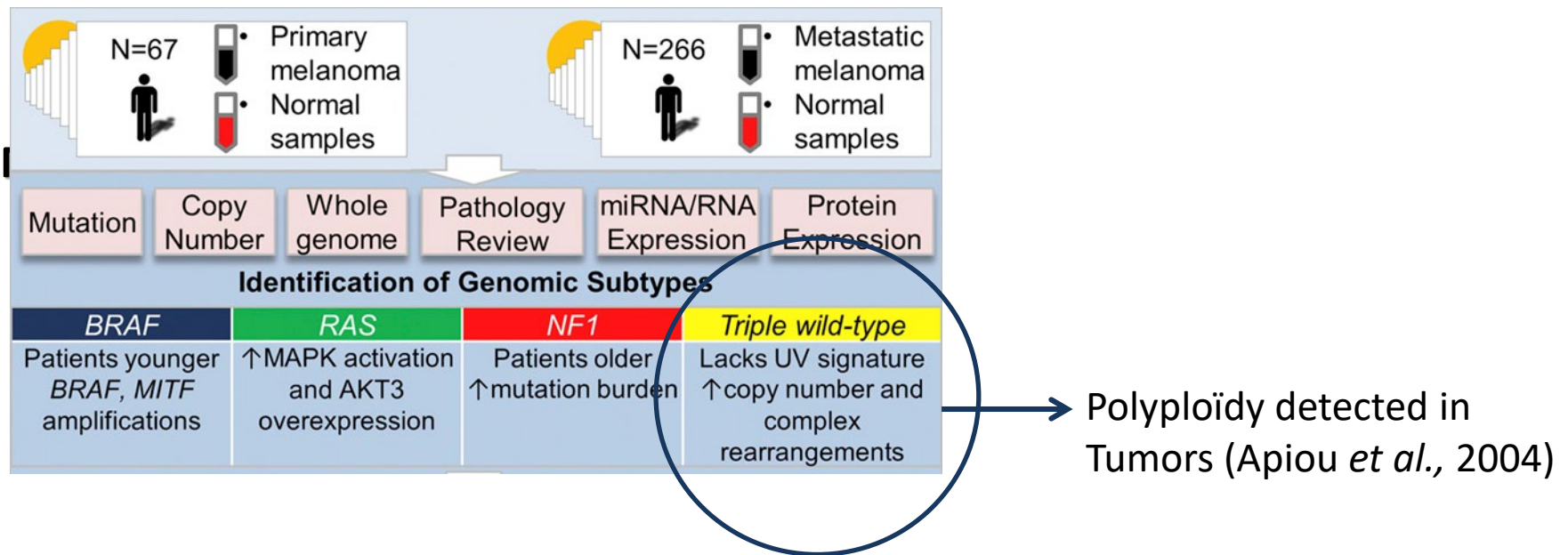
# Survey of driver mutations in Melim tumors

Targeted approach on driver mutations found in human melanoma

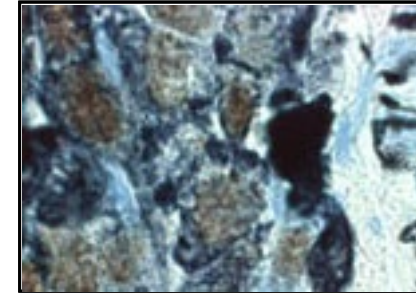
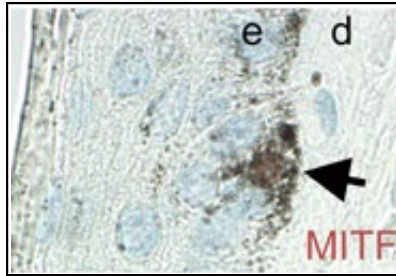
BRAF, NRAS, HRAS, KRAS, NF1, KIT, PTEN, p53 : **no driver mutation identified**

Global approach using exome sequencing of tumor DNA

High mutation rate



# Transcriptome analysis in MeLiM uncovers RACK1 mRNA



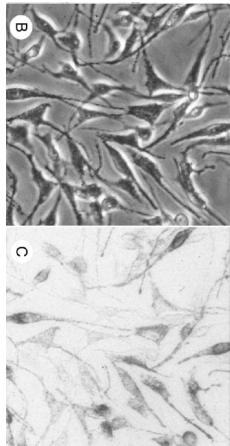
Cell line of epidermal melanocytes : *PigMel*

1<sup>ary</sup> Lung metastases cells from MeLiM melanoma

Serial analysis of gene expression

55 genes differentially expressed ( $p < 0,05$ ):  
G-beta like protein GNB2L1

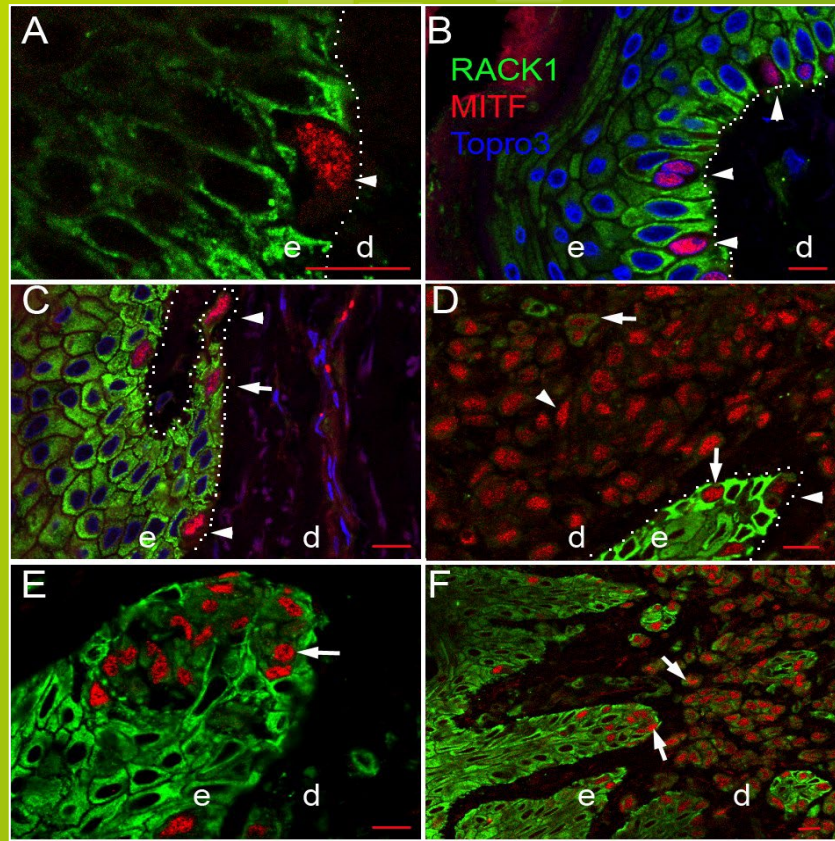
**RACK1** overexpressed in MeLiM melanomas



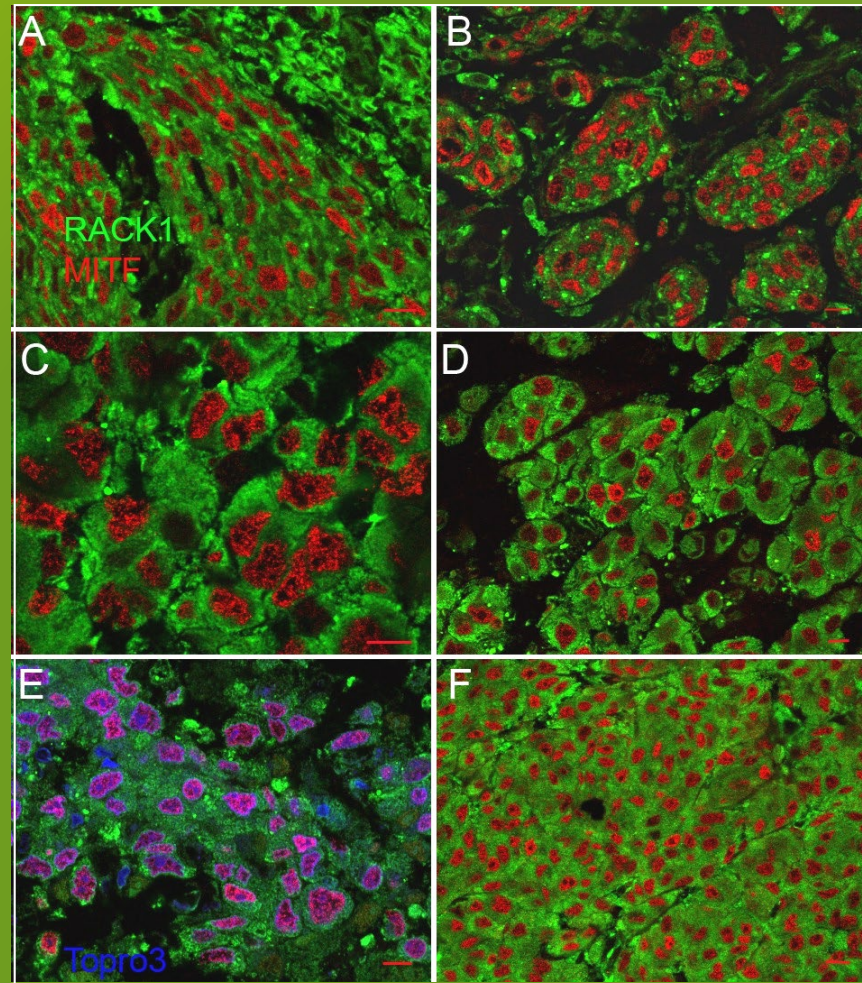
Julé *et al*  
PCR 2003

Egidy *et al*, Molec Cancer 2008

# RACK1 in human nevi and cutaneous melanomas



Egidy *et al*, Molec Cancer 2008



Cutaneous

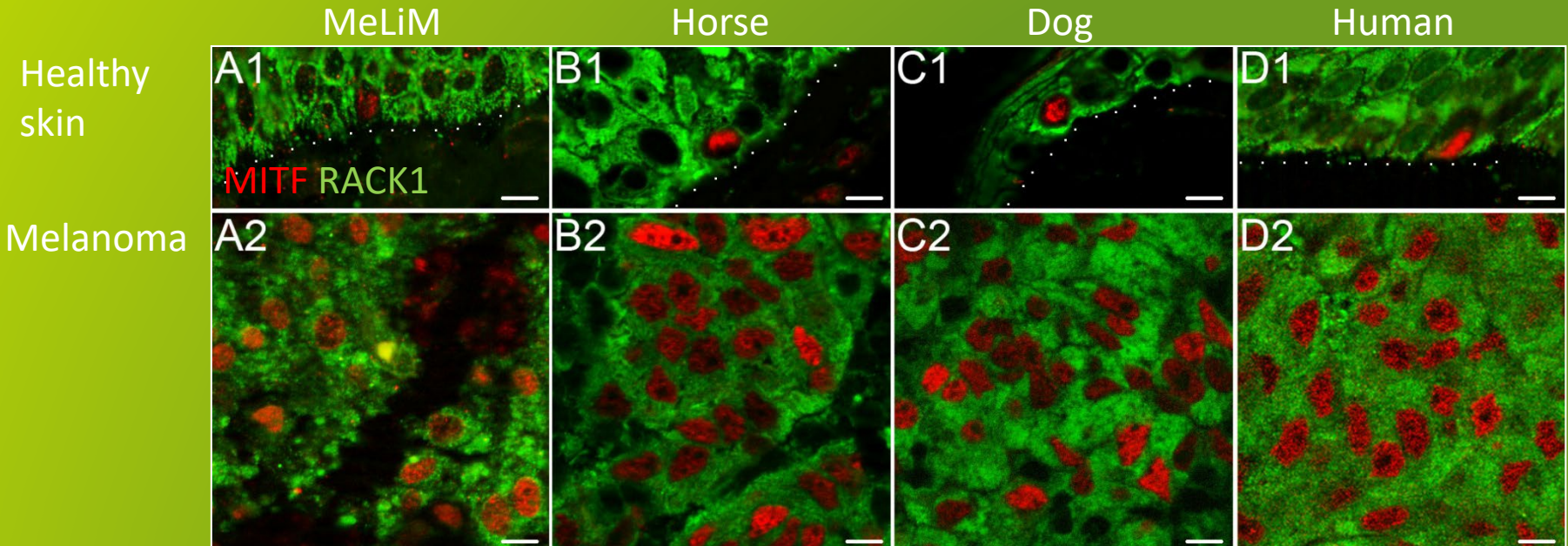
metastasis

□ RACK1 signal is increased in cutaneous and metastatic melanomas

□ RACK1 distribution is homogeneous over malignant lesions

# RACK1, diagnostic marker of cutaneous melanomas

- Conserved distribution pattern in melanomas from 4 species

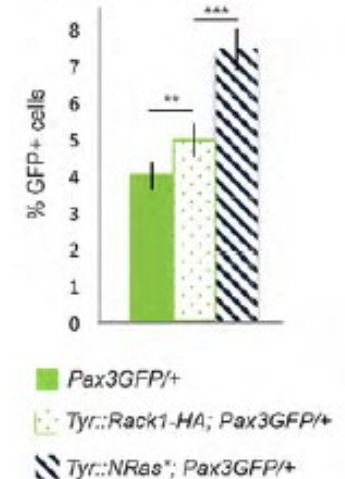
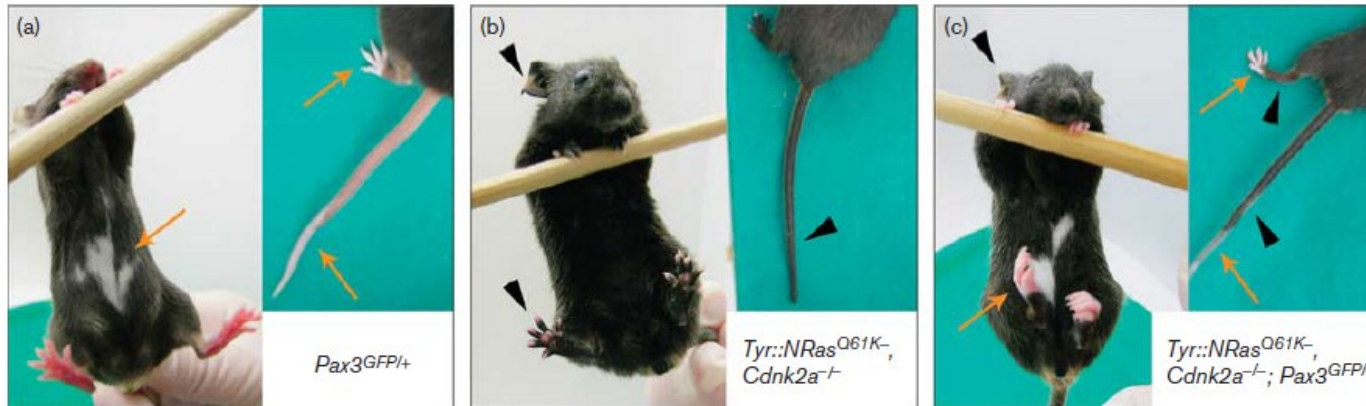
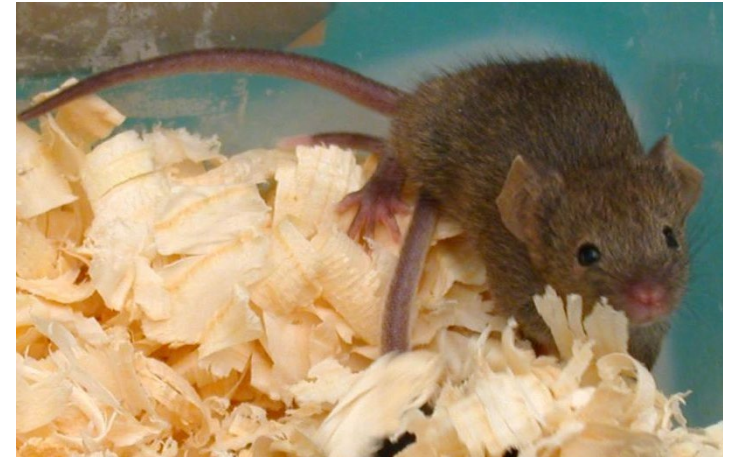


Campagne *et al* BMC Res Vet 2012  
Campagne *et al*, Vet Pathol, 2013

Gene expression profiling in MeLiM led to the identification of RACK1 as potential marker of malignancy for human and veterinary melanocytic proliferations

# Model of RACK1 overexpression targeted to melanocytes

- *Tyr::Rack1-HA; Pax3<sup>GFP/+</sup>* mouse



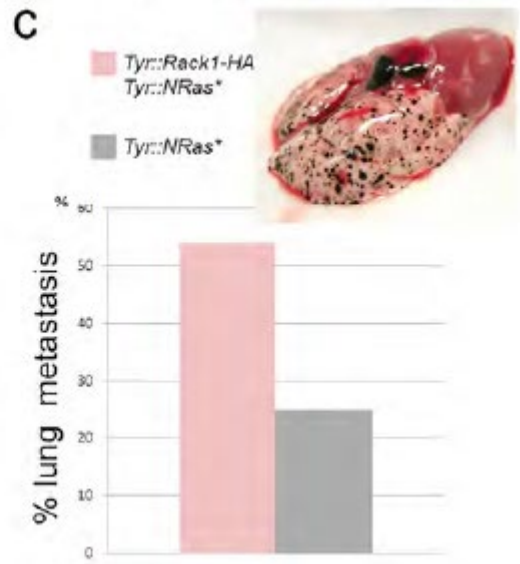
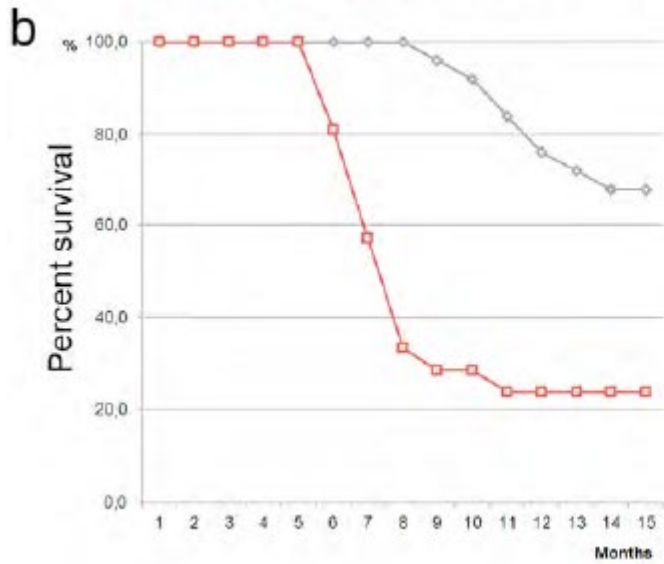
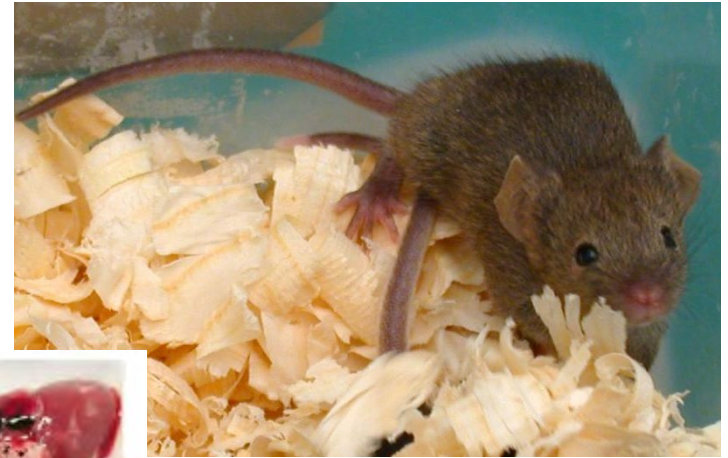
Campagne et al. Melanoma Research 2016

RACK1 overexpression increases neonatal skin melanocyte number

Campagne et al.  
Cell Signaling 2017

# Model of RACK1 overexpression targeted to melanocytes

- *Tyr::Rack1-HA; Pax3<sup>GFP/+</sup>* mouse

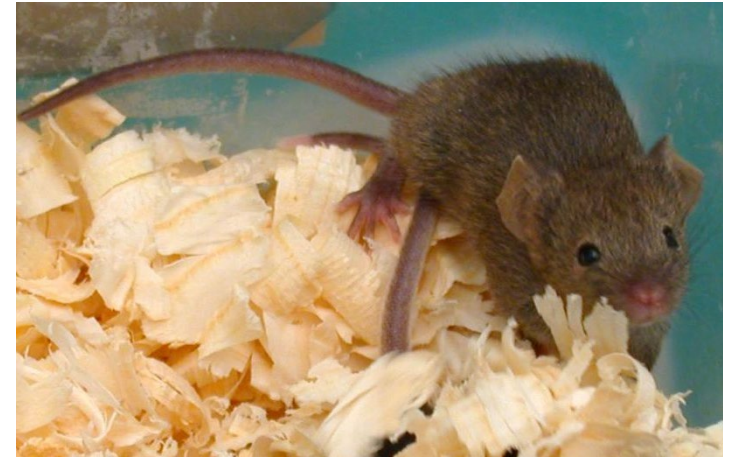


RACK1 accelerates melanoma development

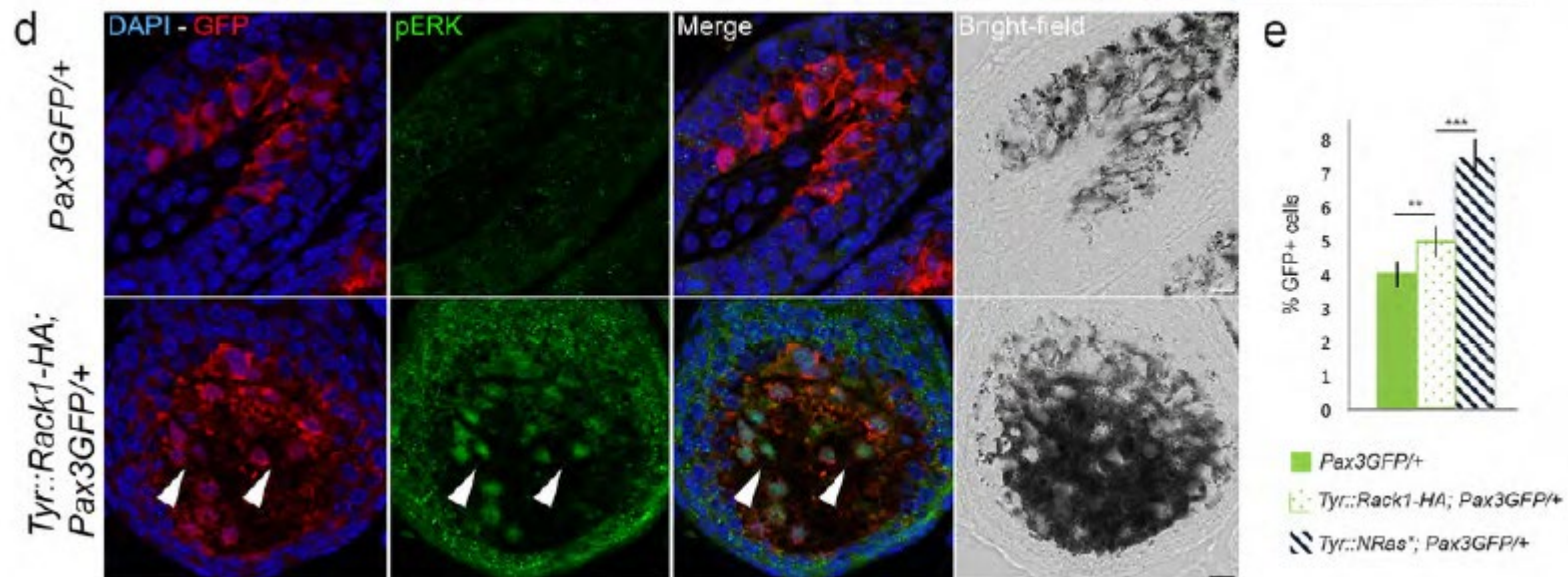
Campagne et al. Cell Signaling 2017

# Model of RACK1 overexpression targeted to melanocytes

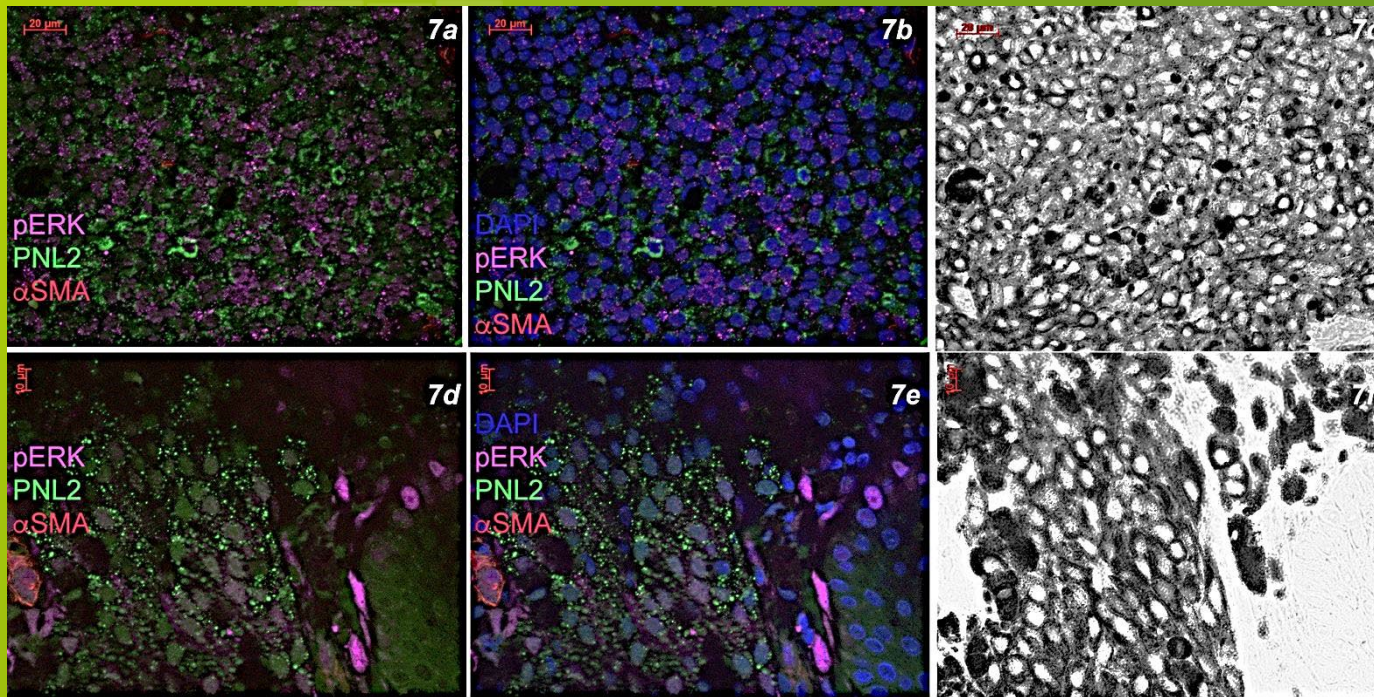
- *Tyr::Rack1-HA; Pax3<sup>GFP/+</sup>* mouse



Campagne et al. Cell Signaling 2017



# Proliferative signaling pathways in MeLiM melanomas



Young tumors  
(pigs <21 days)

«Older» tumors  
(>21 days)

pERK : activation MAPK-ERK pathway

PNL2 : marker of melanocytes/melanoma cells

αSMA : marker of vascular cells

DAPI: nucleus

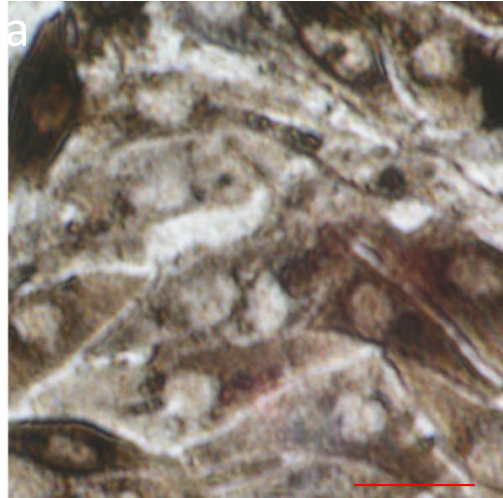
Similar results with pAKT, pJNK (+ other pathways)

→ Proliferation signals activated in young tumors, less as tumors progress

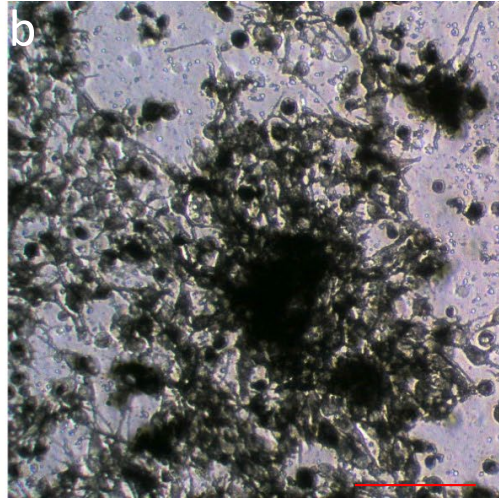


# Malignancy traits in MeLiM melanoma in vitro and xenotransplantation assays

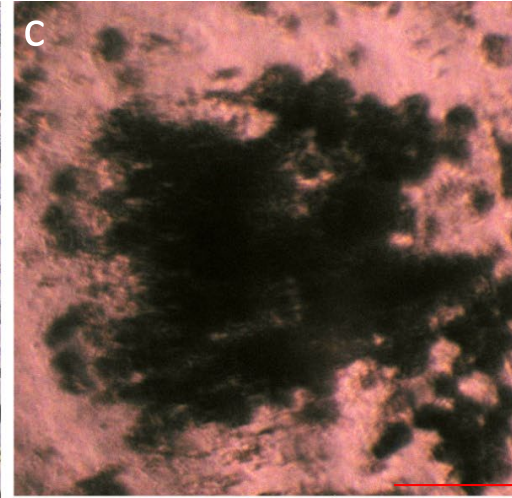
MeLiM melanoma cells in culture Bar:10 $\mu$ m.



Foci at confluent growth 100 $\mu$ m.



Soft agar colony formation 50 $\mu$ m.



➤ **MeLiM melanoma cells are contact insensitive, anchorage independent and serially transplantable in as transformed cells**



# Melanoma development in MeLiM

## Tumoral level



D+7 Growing ulcerated tumor (1 cm)



D+36 Ulcerated exophytic tumor (4 cm)



D+96 Regressed lesion with depigmentation of hair and skin

## Animal level



D+15



D+113



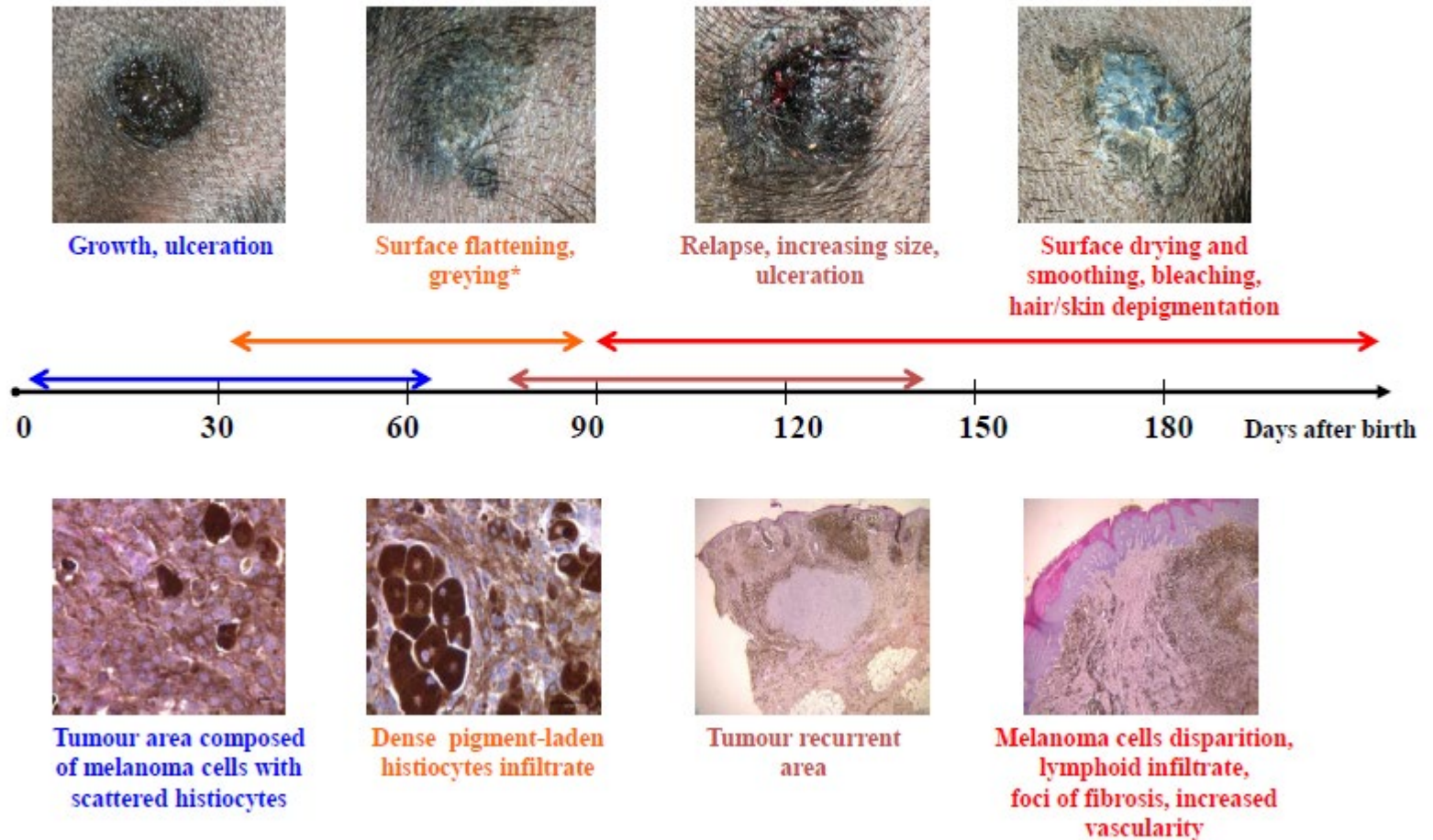
D+214

## Depigmentation

In MeLiM minipigs, melanomas spontaneously regress

Vincent-Naulleau *et al*, PCR 2004

# The MeLiM model : time course of the disease



S. Vincent-Naulleau et al. *Pigment Cell Res.* 2004, 16: 1-12

# Melanoma regression in MeLiM

Spontaneous regression (SR) is defined as the disappearance of the malignant tumor mass without treatment or as a consequence of an indirect action (i.e. treatment against another disease or symptoms) (William Coley, 1891).

Melanomas begin to dry and reduce in size, then become greyish and their surface flattens and smooths

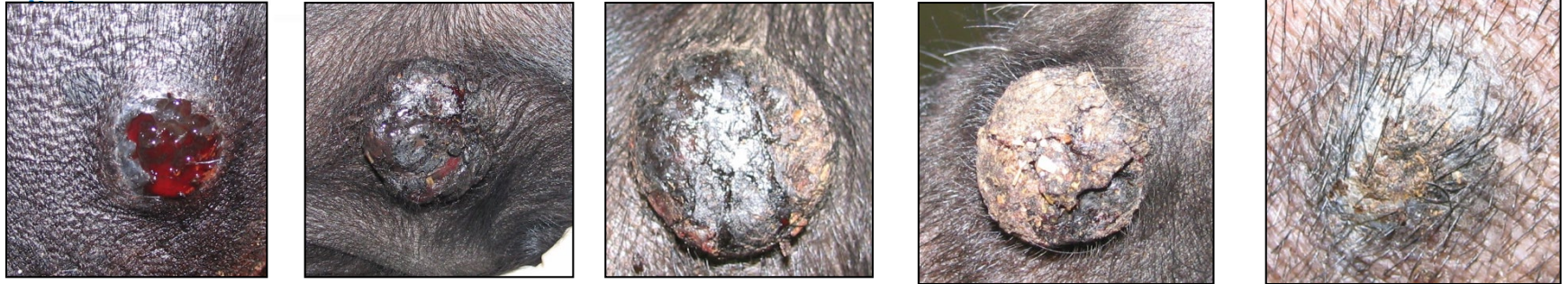
Depigmentation of skin and hair



F. Andreoletti, JJ Leplat, S Vincent-Naulleau INRA-CEA

# Molecular mechanisms of regression

## Clinical phenotypes



$t_0$  (D8)

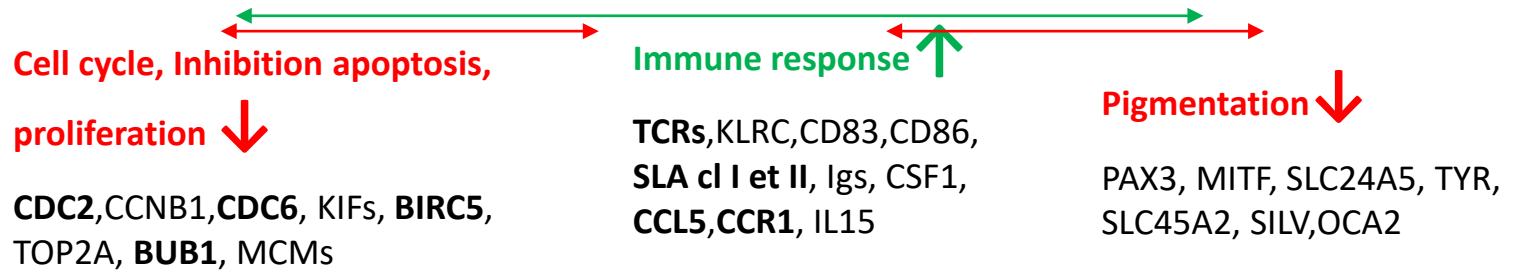
$t_1$  (D28)

$t_2$  (D49)

$t_3$  (D70)

$t_4$  (D91)

[D]



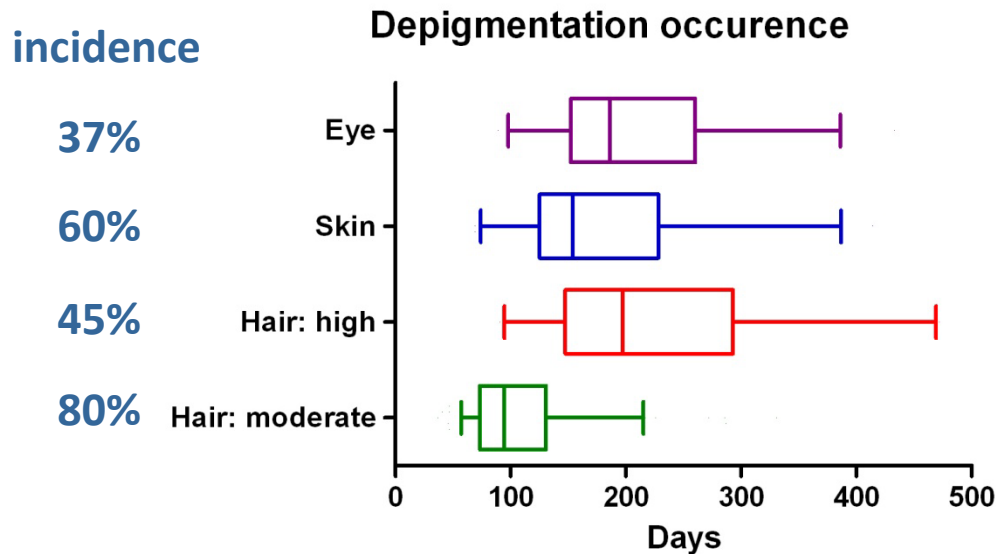
## Array results



Rambow *et al*, Neoplasia 2008

# Depigmentation on MeLiM with melanoma regression

- Follow up of clinical observations on hair, skin, eyes depigmentation in minipigs resembling vitiligo in humans



**No depigmentation**



**Moderate**



**High**

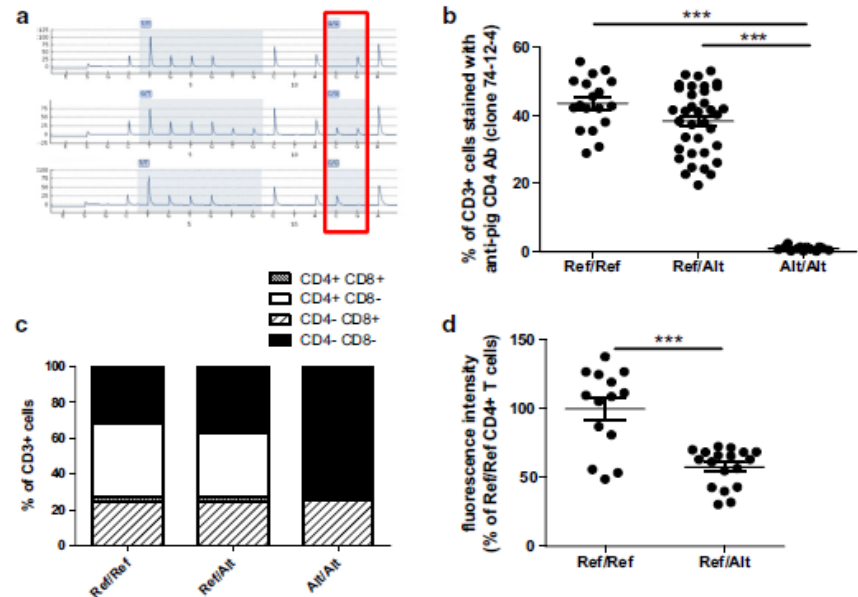
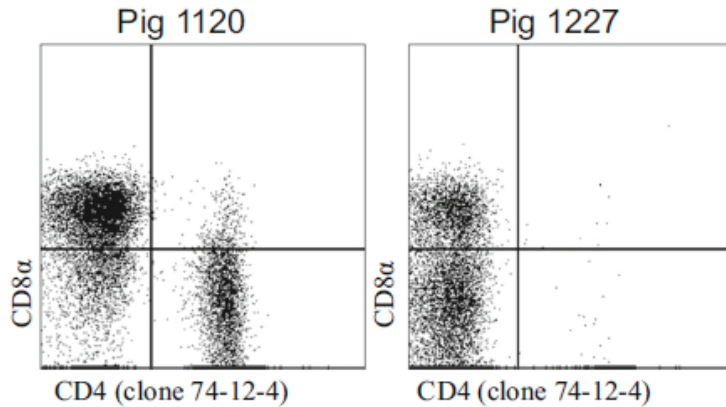
Blanc *et al*, Immunogenetics 2017

# CD4 alleles may loose antibody binding

Some MeLiM did not show CD4 staining

```

Ref Haplo.1  24  GTQEKYLVLGKAGDLAELPCHSSQKKNLFPNWKNSNQTKI LGGHGGSFWHT  72
Ref Haplo.2  24  -----S-----K  72
Ref Haplo.3  24  -----K  72
Alt Haplo    24  -----S---D-I---RS-RNL--K  72
CD4.2       24  -----S---D-I---RS-RNL--K  72
CD4.B       24  -----S---D-I---RS-RNL--K  72
*****,**:* *** .*:**
    
```



A CD4 epitope deficiency is produced by a specific haplotype in MeLiM

# CD4 alleles may loose antibody binding



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## Identification of a Type 1 Diabetes-Associated CD4 Promoter Haplotype with High Constitutive Activity

O. P. Kristiansen, A. E. Karlsen, Z. M. Larsen, J. Johannesen,

F. Pociot, T. Mandrup-Poulsen

The Danish IDDM Epidemiolog

First published: 2 June 2004 Full p



Explore this journal >

## Possible association of the CD4 gene polymorphism with vitiligo population

M. Zamani, M. A. Tabatabaiefar, S. M. P. Mansouri

First published: 19 October 2009 Full publi



ELSEVIER

Veterinary Immunology and Immunopathology

Volume 168, Issues 3–4, 15 December 2015, Pages 176–183



Sundt III,\* David H. Sachs,\* and

## Identification of a CD4 variant in Microminipigs not detectable with available anti-CD4 monoclonal antibodies

Tatsuya Matsubara<sup>a</sup>, Naohito Nishii<sup>a, b, c, d, e</sup>, Satoshi Takashima<sup>b</sup>, Masaki Takasu<sup>a, b</sup>, Noriaki Imaeda<sup>b</sup>, Kayo Aiki-Oshimo<sup>b</sup>, Kazuaki Yamazoe<sup>a, b</sup>, Yoshie Kametani<sup>c</sup>, Asako Ando<sup>c</sup>, Hitoshi Kitagawa<sup>a, b</sup>

BMC Veterinary Research

Open Access



## Identification and characterization of two CD4 alleles in Microminipigs

Tatsuya Matsubara<sup>1,2</sup>, Naohito Nishii<sup>1,2\*</sup>, Satoshi Takashima<sup>2</sup>, Masaki Takasu<sup>1,2</sup>, Noriaki Imaeda<sup>2</sup>, Kayo Aiki-Oshimo<sup>2</sup>, Kazuaki Yamazoe<sup>1,2</sup>, Michinori Kakisaka<sup>3</sup>, Shin-nosuke Takeshima<sup>3</sup>, Yoko Aida<sup>3</sup>, Yoshie Kametani<sup>4</sup>, Jerzy K. Kulski<sup>4,5</sup>, Asako Ando<sup>4</sup> and Hitoshi Kitagawa<sup>1,2</sup>

Animal Biotechnology > Latest Articles

26 Views  
0 CrossRef citations

Original Articles

## Distribution of the CD4 Alleles in Sus scrofa Demonstrates the Genetic Profiles of Western Breeds and Miniature Pigs

Tomoko Eguchi-Ogawa, Tatsuya Matsubara, Daisuke Toki, Naohiko Okumura, Asako Ando, Hitoshi Kitagawa

## A Common CD4 Gene Variant Is Associated with an Increased Risk of HIV-1 Infection in Kenyan Female Commercial Sex Workers

Julius O. Oyugi, Françoise C. M. Vouriot, Judie Alimonti, Stephen Wayne, Ma Luo, Allison M. Land, Zhujun AO, Xiaojian Yao, Rafick P. Sekaly, Lawrence J. Elliott ... Show more

The Journal of Infectious Diseases, Volume 199, Issue 9, 1 May 2009,



# Impact of CD4 haplotypes on depigmentation

a No depigmentation



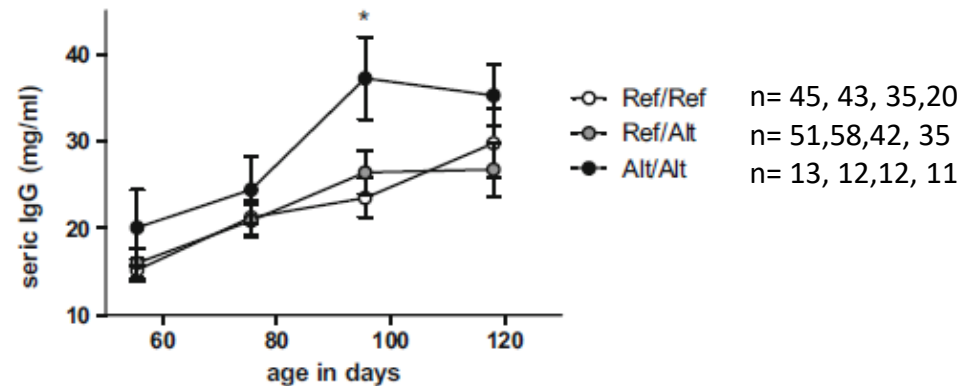
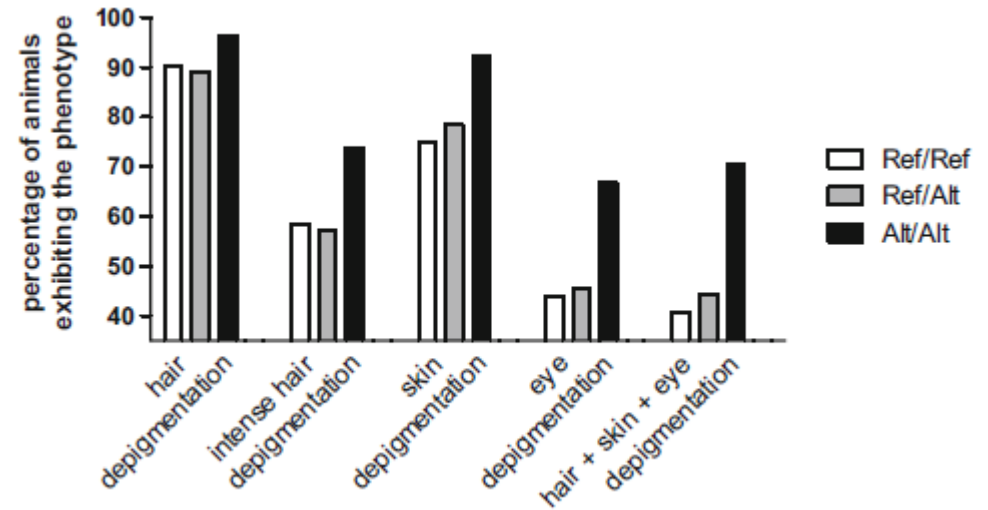
b Moderate depigmentation



c Intense depigmentation



d Skin and eye depigmentation



CD4 is associated with immune response-related phenotypes in MeLiM minipigs

Blanc *et al*, Immunogenetics 2017



## Melanoma regression in MeLiM

- ❖ Longitudinal transcriptomic studies: regression relates to melanoma cell's cell cycle arrest, & an immune reaction
- ❖ Senescence is detected by patches along tumor regression
  - **Regression is partly the result of replicative potential loss in MeLiM**
- ❖ Regression goes along with depigmentation (*CD4* locus specific haplotype)
- ❖ Blood antibodies against porcine melanocytic and melanoma antigens appear during regression
  - **Regression is partly the result of immunoreactivity in MeLiM**



**Patients could not just survive with cancer, but live without cancer**

# **Regression WANTED**

**Characterisation of a minipig spontaneous regression  
model with no invalidating adverse effects  
to find novel pathways of immune activation**

**Is this capacity to regress transposable to human cancer?**



# Characterisation of a minipig spontaneous regression model with no invalidating adverse effects to find novel pathways of immune activation

## Functionally test:

1. whether regression is specific to MeLiM mutations
2. and/or dependent on the immune system
3. Identify novel markers of interaction immune / tumor cells
4. compare to human melanoma cells behaviour

Development and integration of new experimental models relevant for research in oncology: Optimisation of the 3R principle

ORIGINAL ARTICLE

# Targeted inhibition of metastatic melanoma through interference with Pin1-FOXM1 signaling

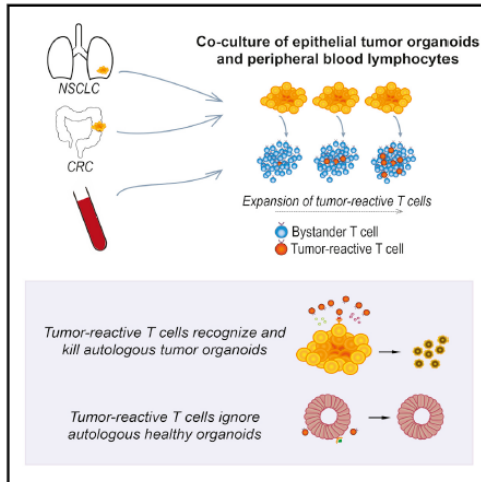
F Kruiswijk<sup>1,8</sup>, SC Hasenfuss<sup>1,8</sup>, R Sivapatham<sup>2,8</sup>, MP Baar<sup>3</sup>, D Putavet<sup>3</sup>, KAT Naipal<sup>3</sup>, NJF van den Broek<sup>1</sup>, W Kruit<sup>4</sup>, PJ van der Spek<sup>5</sup>, DC van Gent<sup>3</sup>, AB Brenkman<sup>1,6</sup>, J Campisi<sup>2,7</sup>, BMT Burgering<sup>1</sup>, JHJ Hoeijmakers<sup>3</sup> and PLJ de Keizer<sup>1,2,3</sup>

Resource

Cell

## Generation of Tumor-Reactive T Cells by Co-culture of Peripheral Blood Lymphocytes and Tumor Organoids

Graphical Abstract



Authors

Krijn K. Dijkstra, Chiara M. Cattaneo, Fleur Weeber, ..., Hans Clevers, Ton N. Schumacher, Emile E. Voest

Correspondence

e.voest@nki.nl

In Brief

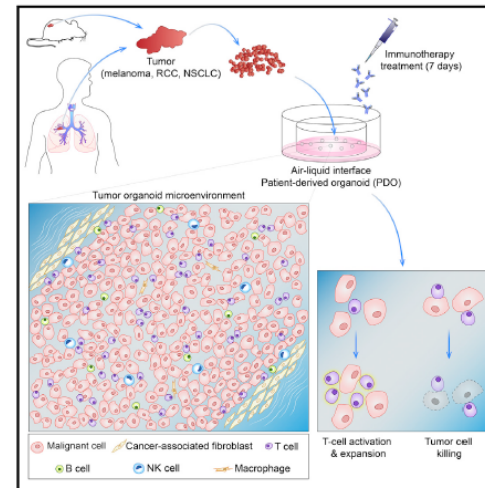
A modified patient-derived tumor organoids system allows the expansion of tumor-specific T cells from blood for personalized analysis of their anti-cancer properties.

Resource

Cell

## Organoid Modeling of the Tumor Immune Microenvironment

Graphical Abstract



Authors

James T. Neal, Xingnan Li, Junjie Zhu, ..., Grace X.Y. Zheng, Mark M. Davis, Calvin J. Kuo

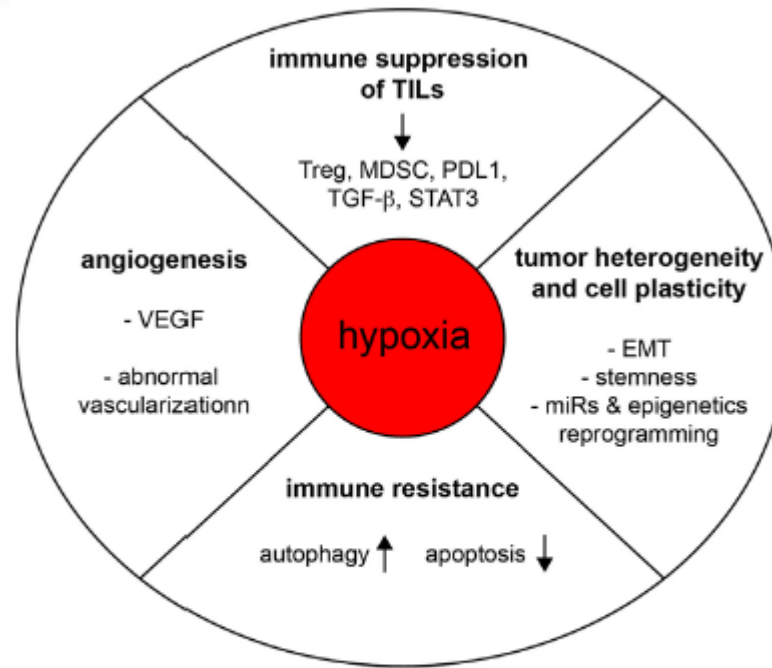
Correspondence

cjkuo@stanford.edu

In Brief

The tumor-immune microenvironment is modeled using a patient-derived organoid approach that preserves the original tumor T cell receptor spectrum and successfully models immune checkpoint blockade.

# Hypoxia subverts the immune system and promotes tumor progression via HIF and STAT3



**FIGURE 2 |** Hypoxia subverts the function of the immune system and promotes tumorigenesis. Hypoxia regulates tumor progression through various mechanisms of action, including the promotion of angiogenesis, tumor heterogeneity, cell plasticity, immune resistance, and intratumoral immune suppression.

Terry et al Front Immunol 2017

# Conclusions and perspectives

- Minipigs are medium size animal models with many features similar to humans
- Melanoma in MeLiM minipigs is genetically heterogeneous as in humans
- Mechanisms of tumour progression share genetic, histological and biochemical signatures with human triple wild type melanomas
- Efficient spontaneous tumour regression seems related to innate and acquired immunity pathways
- study of few non regressing MeLiM tumours on autonomous capacity to proliferate, senesce or die, and on immune activation are ongoing

Patients could not just survive with cancer, but live without cancer

# Animal research is regulated





Since 1951, the Animal Welfare Institute has been dedicated to reducing animal suffering caused by people.

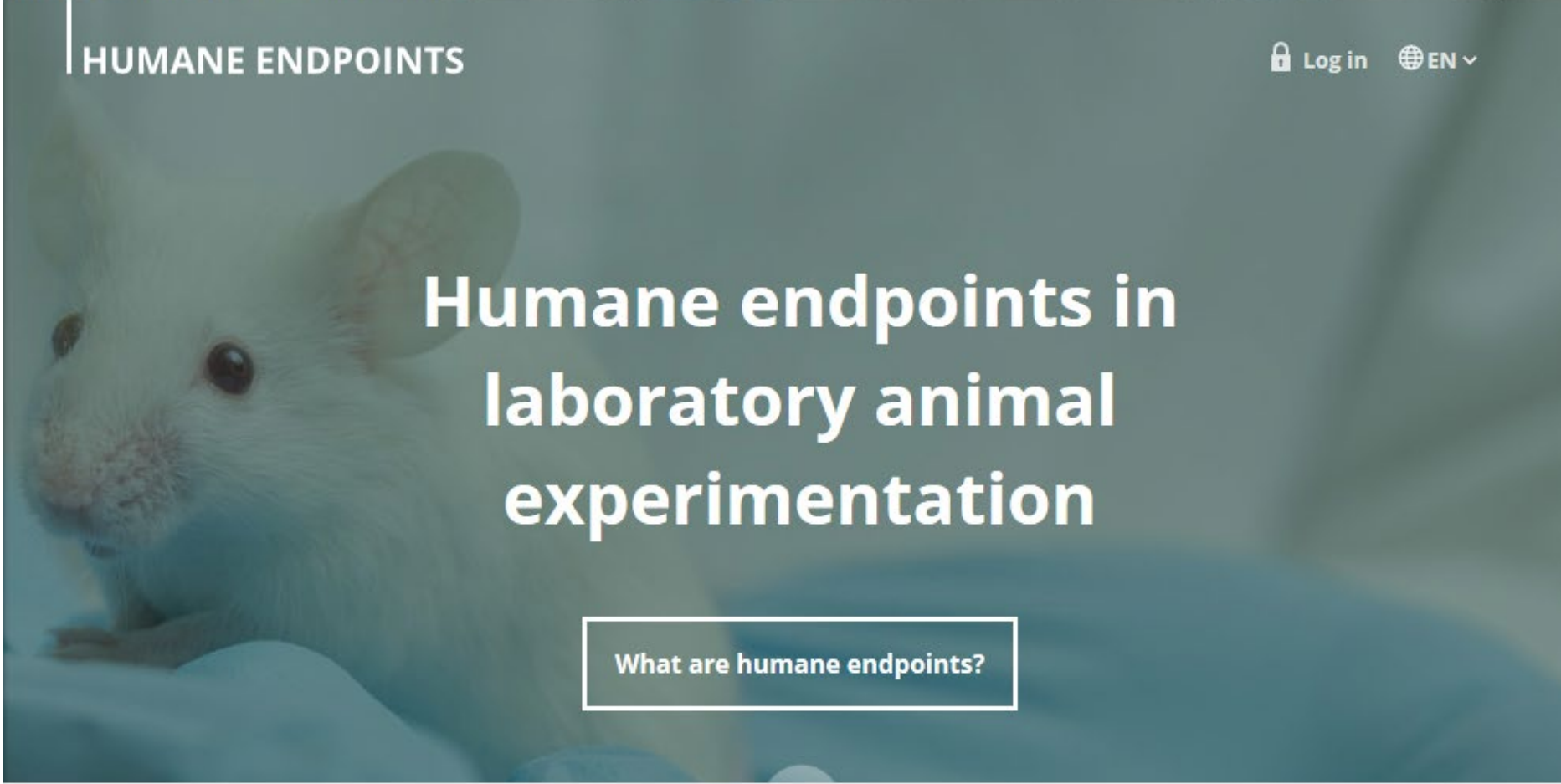
We seek better treatment of animals everywhere— in the laboratory, on the farm, in commerce, at home, and in the wild.

## EXECUTIVE SUMMARY

### Background

EU citizens are becoming increasingly concerned that all kinds of production systems and other activities should be sustainable. Animal welfare is an important aspect of sustainability, and also of product quality, and may result in consumers refusing to buy products. The welfare of an individual is its state as regards its attempts to cope with its environment. Welfare includes feelings and health and can be measured scientifically. It is a biological concept, quite different from rights, and refers only to living animals.

The terms welfare, stress, needs, humane and euthanasia are defined and some of the ways in which they are used imprecisely in EU documents and elsewhere are described. Animal health is principally of importance because it is a key part of animal welfare. It can also have economic and human disease consequences. The terms health and welfare have exactly the same meaning for humans and for other animal species, hence the current interest in 'one health' and 'one welfare'. When the welfare of individuals is poor, there is increased susceptibility to disease, hence improving welfare generally reduces disease. Preventing anti-microbial resistance is good for animal welfare and improved welfare can reduce the need for use of anti-microbial products. Those with a medical background and those with a veterinary or other biological background benefit from exchanging information, in particular because of the similarities in disease and in other causes of poor welfare in humans and other species. Care for people and care for animals used by people is generally better if all are considered as individuals.



# Humane endpoints in laboratory animal experimentation

What are humane endpoints?



## EXPERIMENTATION ANIMALE

### RESSOURCES

*Le dispositif  
d'expérimentation  
animale*

### REGLEMENTATION

*La réglementation  
sur l'expérimentation  
animale*

### DAP

*Comment faire une  
demande d'autorisation  
de projet?*

### COMETHEA

*Comité d'éthique  
en expérimentation  
animale*

### CELLULE ANIMALIERS

*Le réseau  
des  
animaliers*

### LIENS

*S'informer  
et suivre  
l'actualité*

# What are humane endpoints?

A humane **endpoint** can be defined as:

**'the earliest indicator in an animal experiment of (potential) **pain** and/or **distress** that, within the context of moral justification and scientific endpoints to be met, can be used to avoid or limit pain and/or distress by taking actions such as humane killing or terminating or alleviating the pain and distress'** (Hendriksen)

Some elements of this definition can

- **'...potential pain...'** (Hendrikse) e.g. pre-clinical parameters such as up/down regulations as an indicator of physiological parameters such as
- **'...within the context of the scientific endpoints'** should always be balanced against the scientific endpoints to be met
- **'...taking actions such as...'** (CC) actions such as humane killing or terminating or alleviating a painful/stressful procedure are

The following conclusions can be drawn from this definition. A humane endpoint :

- Not necessarily means the humane killing of the animal, but could also result in interventions to alleviate the stressful/painful experimental procedure (e.g. performing surgery) or providing **analgesics**.
- Is not necessarily based on clinical signs but could also start from pre-clinical signs or from physiological or molecular biomarkers predictive of pain/distress later on in the disease process.
- Should be balanced against the scientific endpoints to be met. Thus, pain and distress might be intrinsic to a certain experimental model (e.g. **arthritis**). However, in this case the humane endpoint should never be beyond the scientific endpoint.
- Should never be beyond the level of moral justification.

A humane endpoint can be considered as a possible **refinement** alternative for those experiments that involve pain and **discomfort** to the animals. In the Netherlands annually about 2.7 percent of all animals used in research experience more than 'moderate/severe' (Zo Doende 2014, an annual report of the Netherlands Food and Consumer Product Safety Authority, only in Dutch).

Biomedical research areas with relatively high percentages of pain and distress are **cancer** research, toxicity studies, vaccine potency studies, infectious disease studies and autoimmune disease studies.

Applying humane endpoints should seriously be considered when animal experiments involve severe pain and **suffering**.

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INRA -Get-PlaGE

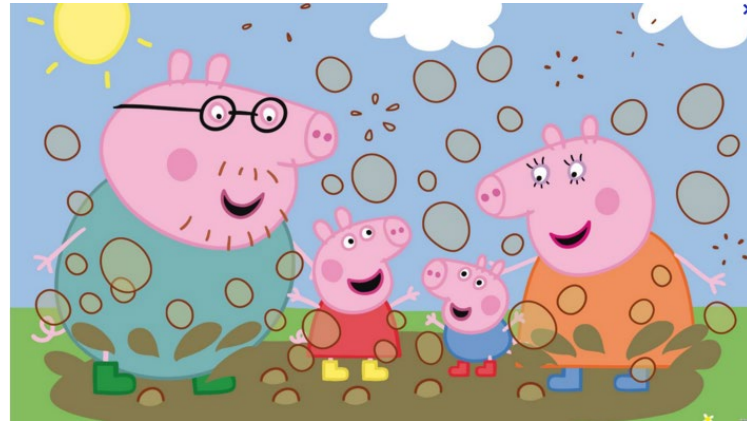
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Salem Chouaib

Stéphane Terry






Please, split in 2 groups

- Swine experimental Unit
- Histology facility

Pascal Lafaux

Julie Rivière  
Marthe Vilotte

Interested? Mail [Giorgia.egidy-maskos@inra.fr](mailto:Giorgia.egidy-maskos@inra.fr)

A fluorescence microscopy image of plant tissue, likely a leaf cross-section. The image shows a dense network of cells. The green signal highlights the cell walls and chloroplasts, while the red signal is concentrated in the nuclei, and the blue signal is distributed throughout the cells, possibly representing a specific protein or another organelle. The overall appearance is a complex, interconnected pattern of these three colors.

Thank you for your attention